FIG. 9

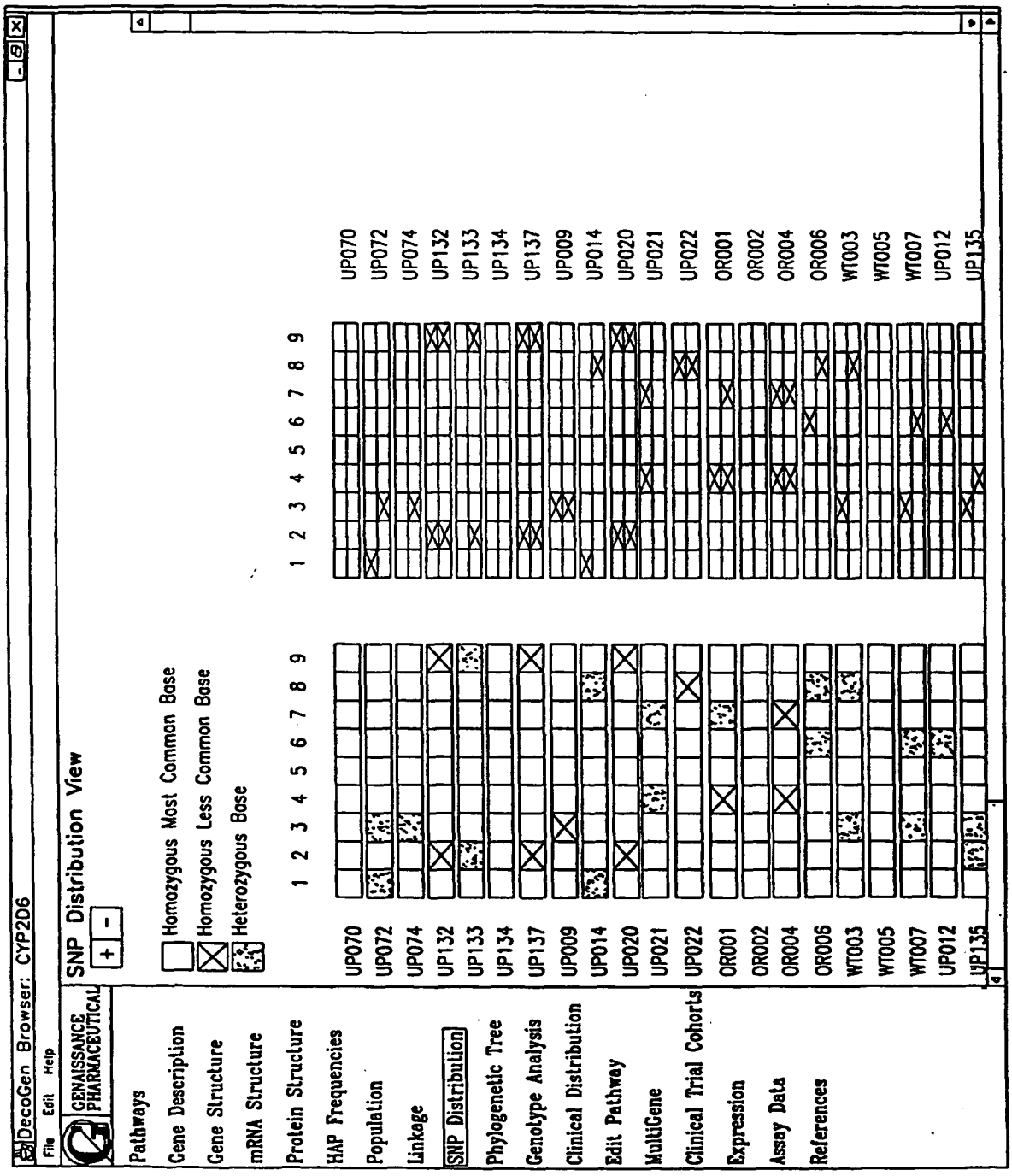

DecoGen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
SNP Distribution View
Homozygous Most Common Base
Homozygous Less Common Base
Heterozygous Base
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References
1 2 3 4 5 6 7 8 9
UP070
UP072
UP074
UP132
UP133
UP134
UP137
UP009
UP014
UP020
UP021
UP022
OR001
OR002
OR004
OR006
WT003
WT005
WT007
UP012
UP135

FIG. 10

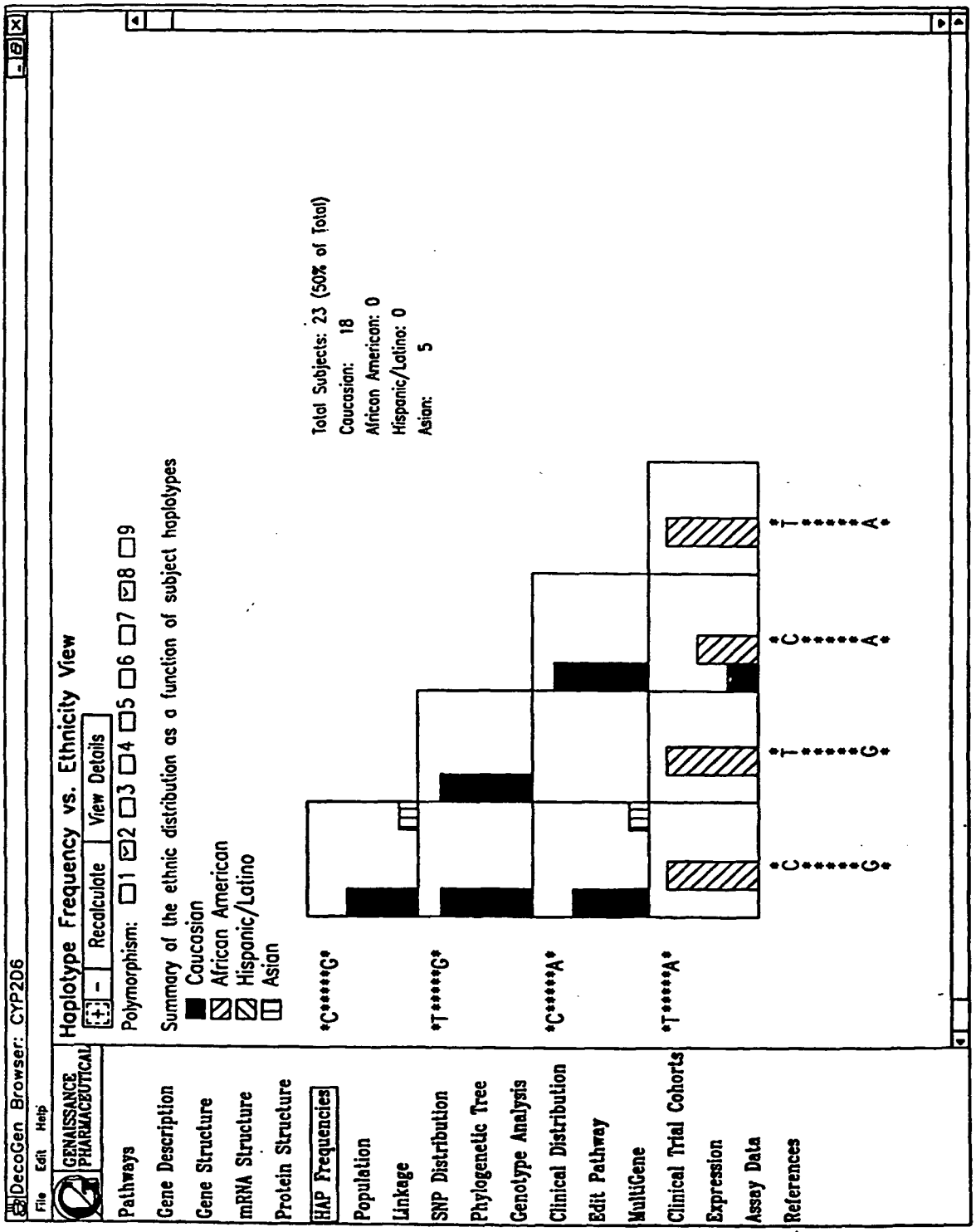

DecoGen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Haplotype Frequency vs. Ethnicity View
Recalculate
View Details
Polymorphism: 1 2 3 4 5 6 7 8 9
Summary of the ethnic distribution as a function of subject haplotypes
Caucasion
African American
Hispanic/Latino
Asian
Total Subjects: 23 (50% of Total)
Caucasion: 18
African American: 0
Hispanic/Latino: 0
Asian: 5
*C*****G*
*T*****G*
*C*****A*
*T*****A*
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References

FIG. 11

DecoGen Browser: CYP2D6

File Edit Help

GENAISSANCE PHARMACEUTICALS

Haplotype Frequency vs. Ethnicity View

+ - Recalculate View Summary

Polymorphism: ☐1 ☑2 ☐3 ☐4 ☐5 ☐6 ☐7 ☑8 ☐9

Pathways

Gene Description

Gene Structure

mRNA Structure

Protein Structure

HAP Frequencies

Population

Linkage

SNP Distribution

Phylogenetic Tree

Genotype Analysis

Clinical Distribution

Edit Pathway

MultiGene

Clinical Trial Cohorts

Expression

Assay Data

References

Details of the ethnic distribution as a function of subject haplotypes

3 Columns are given for each Ethnogeographic group:
Total number sampled with HAP pair
Fraction of the ethnogeographic group with that HAP pair
Fraction expected under Hardy-Weinberg equilibrium for that HAP pair

HAP 1	HAP 2	N	%Pop.	Caucasion			African American			Hispanic/Latino			As
*C******G*	*C******G*	23	50%	18	56.3%	37.9%	0	0.0%	0.6%	0	0.0%	0.0%	5
*T******G*	*C******G*	2	4%	2	6.3%	18.9%	0	0.0%	2.4%	0	0.0%	0.0%	0
*T******G*	*T******G*	4	8%	4	12.5%	2.4%	0	0.0%	2.4%	0	0.0%	0.0%	0
*C******A*	*C******G*	5	10%	4	12.5%	25.2%	0	0.0%	2.4%	0	0.0%	0.0%	1
*C******A*	*C******A*	3	6%	3	9.4%	4.2%	0	0.0%	2.4%	0	0.0%	0.0%	0
*T******A*	*C******G*	1	2%	0	0.0%	3.2%	1	12.5%	9.5%	0	0.0%	0.0%	0
*T******A*	*T******G*	2	4%	0	0.0%	0.8%	2	25.0%	18.9%	0	0.0%	0.0%	0
*T******A*	*C******A*	3	6%	1	3.1%	1.1%	2	25.0%	18.9%	0	0.0%	0.0%	0
*T******A*	*T******A*	3	6%	0	0.0%	0.1%	3	37.5%	37.9%	0	0.0%	0.0%	0

FIG. 12

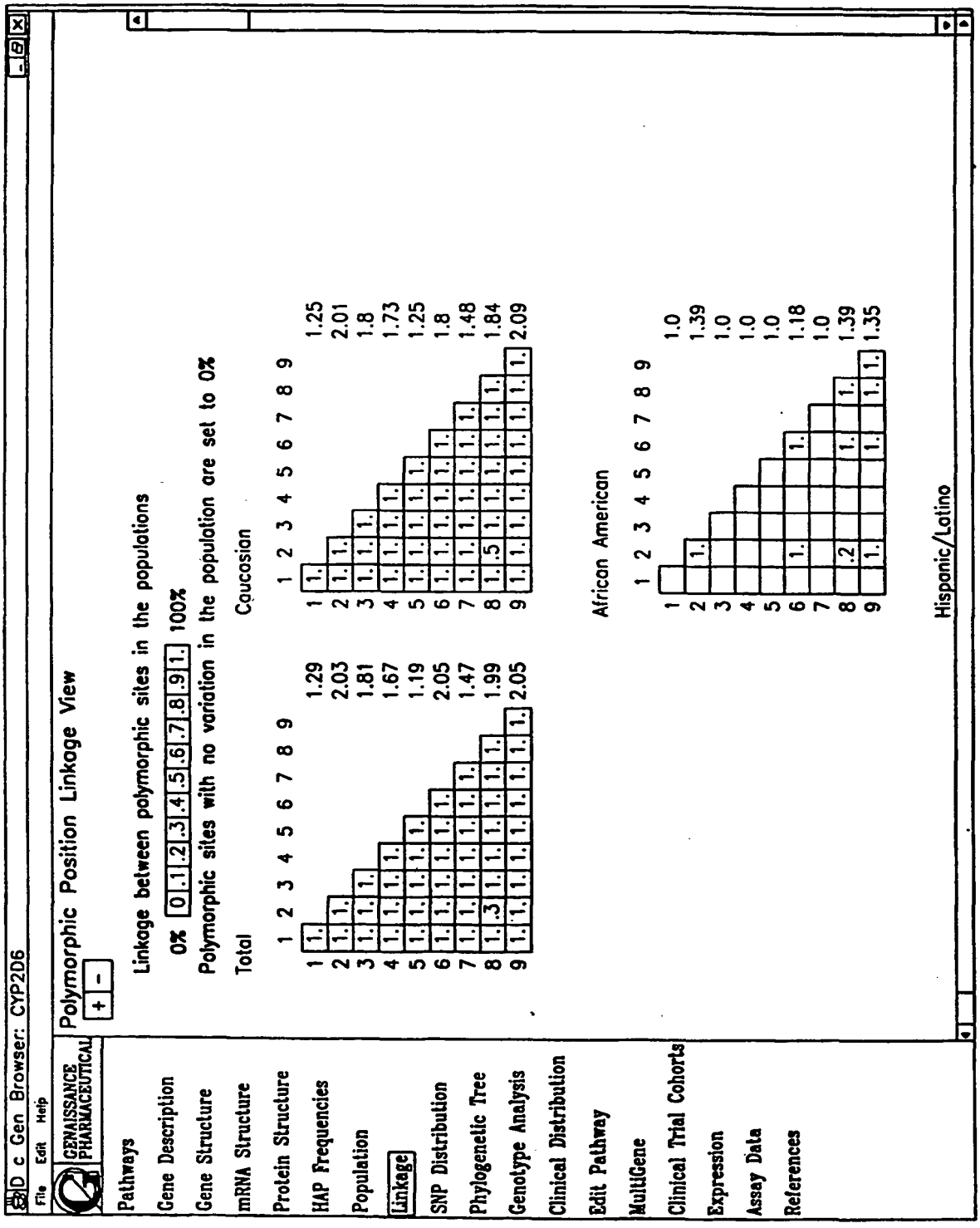

D c Gen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References
Polymorphic Position Linkage View
+ -
Linkage between polymorphic sites in the populations
0% 0 .1 .2 .3 .4 .5 .6 .7 .8 .9 1. 100%
Polymorphic sites with no variation in the population are set to 0%
Total
1 2 3 4 5 6 7 8 9
1 1.
2 1. 1. 1.29
3 1. 1. 1. 2.03
4 1. 1. 1. 1. 1.81
5 1. 1. 1. 1. 1. 1.67
6 1. 1. 1. 1. 1. 1. 1.19
7 1. 1. 1. 1. 1. 1. 1. 2.05
8 1. 1. 1. 1. 1. 1. 1. 1. 1.47
9 1. .3 1. 1. 1. 1. 1. 1. 1. 1.99
1. 1. 1. 1. 1. 1. 1. 1. 1. 2.05
Caucosion
1 2 3 4 5 6 7 8 9
1 1. 1.25
2 1. 1. 2.01
3 1. 1. 1. 1.8
4 1. 1. 1. 1. 1. 1.73
5 1. 1. 1. 1. 1. 1. 1.25
6 1. 1. 1. 1. 1. 1. 1. 1.8
7 1. 1. 1. 1. 1. 1. 1. 1. 1.48
8 1. .5 1. 1. 1. 1. 1. 1. 1. 1.84
9 1. 1. 1. 1. 1. 1. 1. 1. 1. 2.09
African American
1 2 3 4 5 6 7 8 9
1 1.0
2 1. 1.39
3 1. 1.0
4 1. 1.0
5 1. 1.0
6 1. 1. 1.18
7 1. 1.0
8 .2 1. 1. 1.39
9 1. 1. 1. 1. 1.35
Hispanic/Latino

FIG. 13

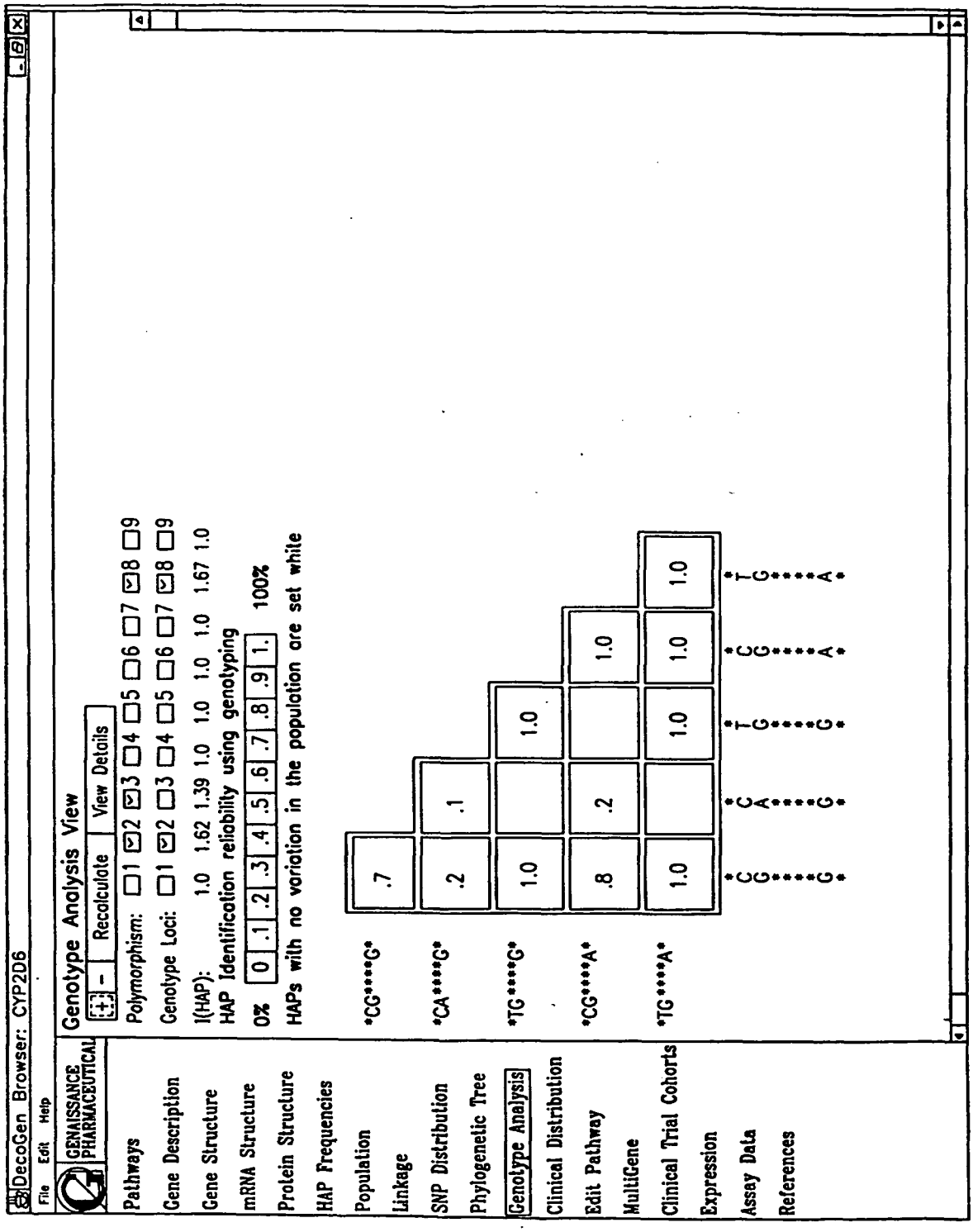

DecoGen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Genotype Analysis View
Recalculate
View Details
Polymorphism: 1 2 3 4 5 6 7 8 9
Genotype Loci: 1 2 3 4 5 6 7 8 9
I(HAP): 1.0 1.62 1.39 1.0 1.0 1.0 1.0 1.0 1.67 1.0
HAP Identification reliability using genotyping
0% 0 .1 .2 .3 .4 .5 .6 .7 .8 .9 1. 100%
HAPs with no variation in the population are set while
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References
*CG****G*
*CA****G*
*TG****G*
*CG****A*
*TG****A*
.7
.2
.1
1.0
.8
.2
1.0
1.0
1.0
1.0
1.0
*C G****G*
*C A****G*
*T G****G*
*C G****A*
*T G****A*

FIG. 14

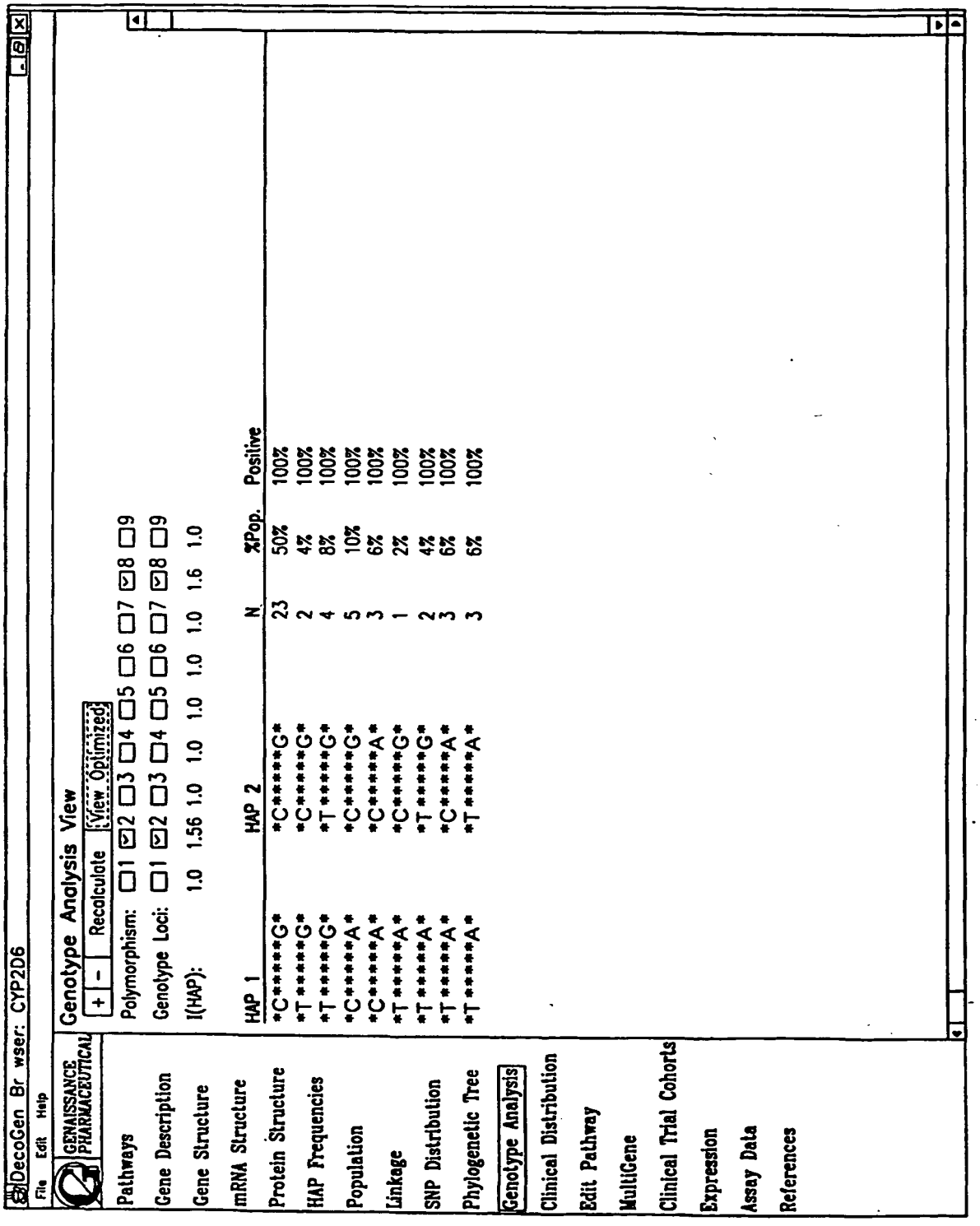

DecoGen Br wser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Genotype Analysis View
+ - Recalculate View Optimized
Polymorphism: 1 2 3 4 5 6 7 8 9
Genotype Loci: 1 2 3 4 5 6 7 8 9
I(HAP): 1.0 1.56 1.0 1.0 1.0 1.0 1.0 1.6 1.0
HAP 1 HAP 2 N %Pop. Positive
*C*****G* *C*****G* 23 50% 100%
*T*****G* *C*****G* 2 4% 100%
*T*****G* *T*****G* 4 8% 100%
*C*****A* *C*****G* 5 10% 100%
*C*****A* *C*****A* 3 6% 100%
*T*****A* *C*****G* 1 2% 100%
*T*****A* *T*****G* 2 4% 100%
*T*****A* *C*****A* 3 6% 100%
*T*****A* *T*****A* 3 6% 100%
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References

FIG. 15

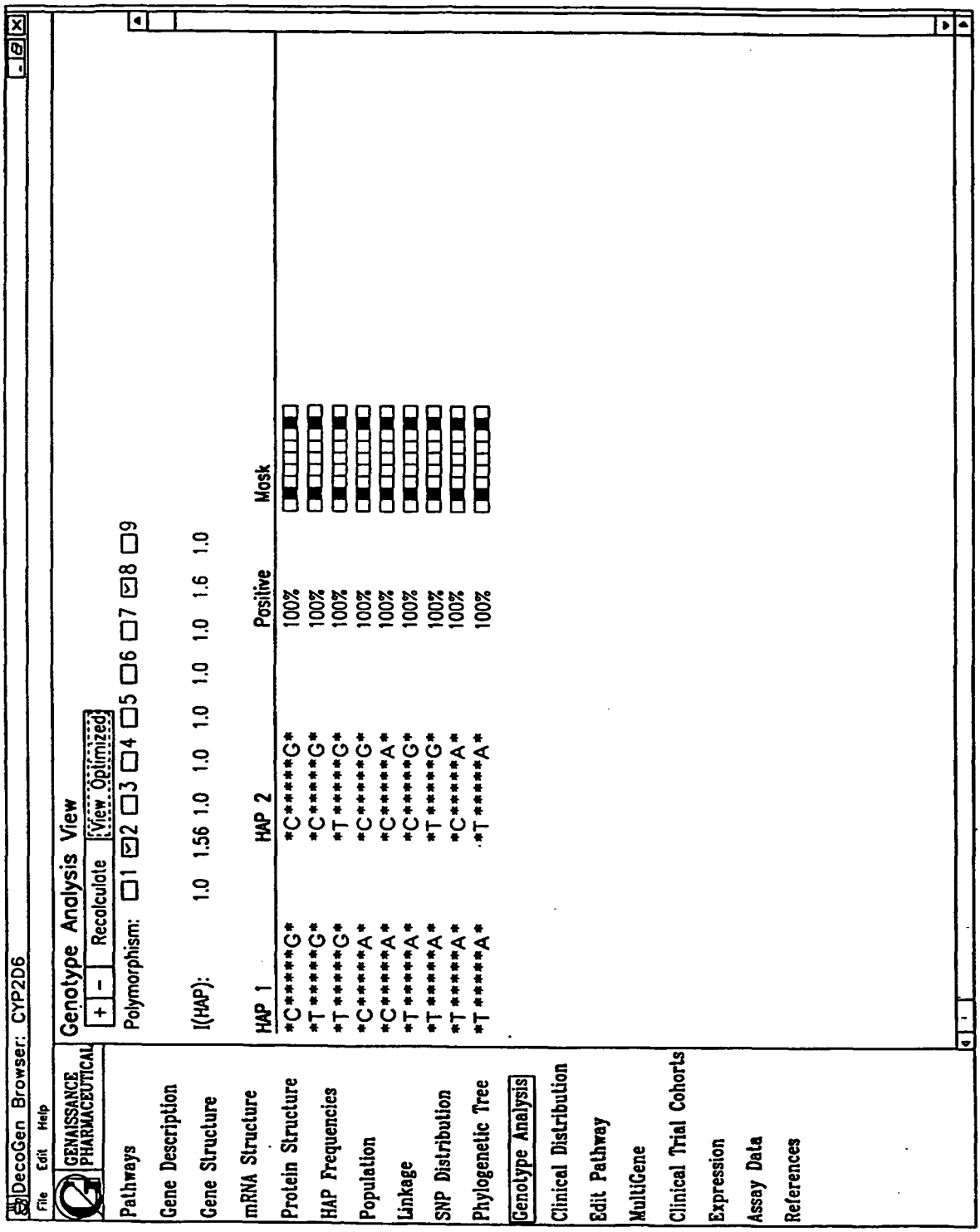

DecoGen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Genotype Analysis View
+ - Recalculate View Optimized
Polymorphism: 1 2 3 4 5 6 7 8 9
I(HAP): 1.0 1.56 1.0 1.0 1.0 1.0 1.0 1.6 1.0
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References
HAP 1
HAP 2
Posilive
Mask
*C*****G*
*C*****G* 100%
*T*****G*
*C*****G* 100%
*T*****G*
*T*****G* 100%
*C*****A*
*C*****G* 100%
*C*****A*
*C*****A* 100%
*T*****A*
*C*****G* 100%
*T*****A*
*T*****G* 100%
*T*****A*
*C*****A* 100%
*T*****A*
*T*****A* 100%

FIG. 16

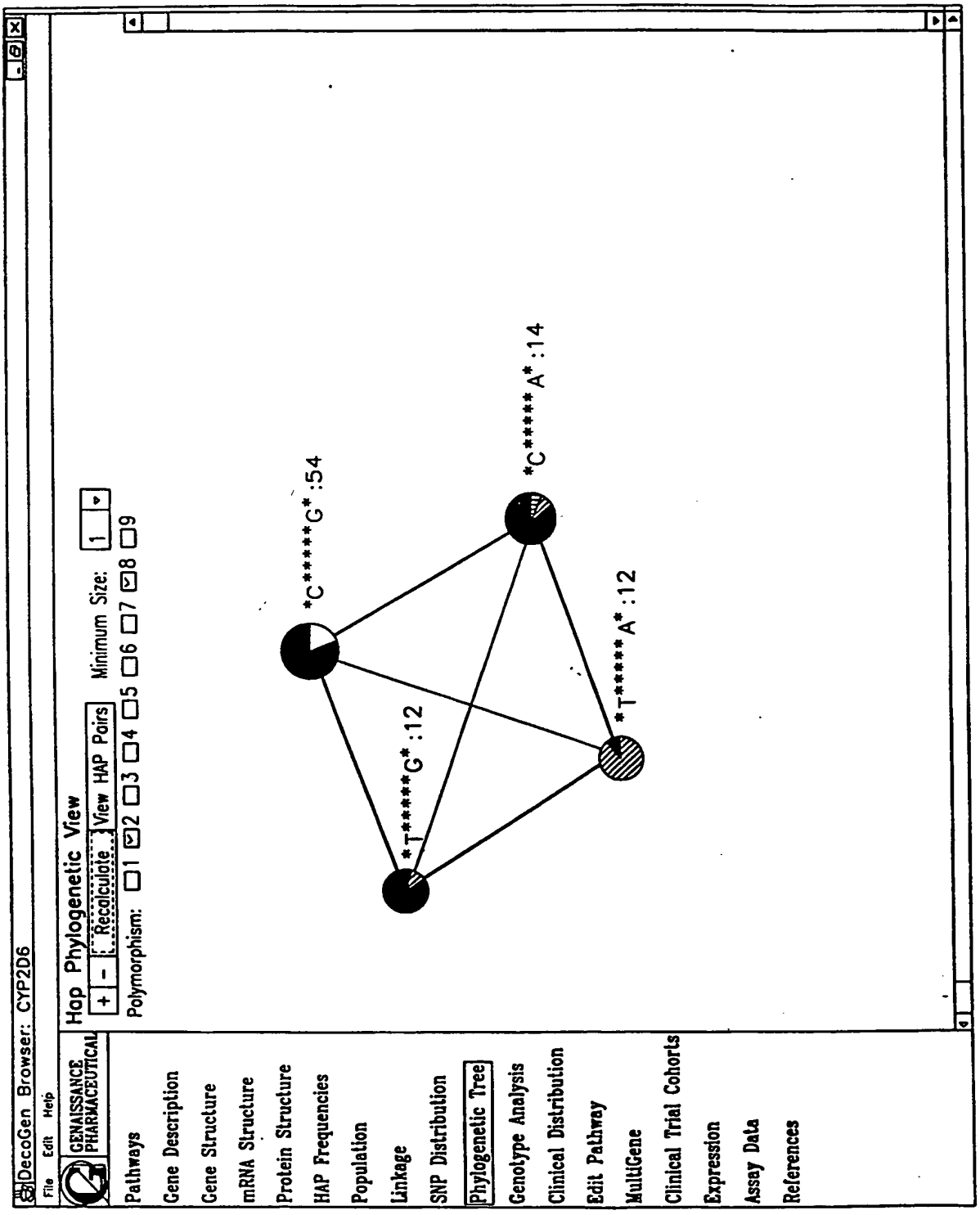

DecoGen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Hap Phylogenetic View
+ - Recalculate View HAP Pairs
Minimum Size: 1
Polymorphism: 1 2 3 4 5 6 7 8 9
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References
*C*****G*:54
*C*****A*:14
*T*****G*:12
*T*****A*:12

FIG. 17

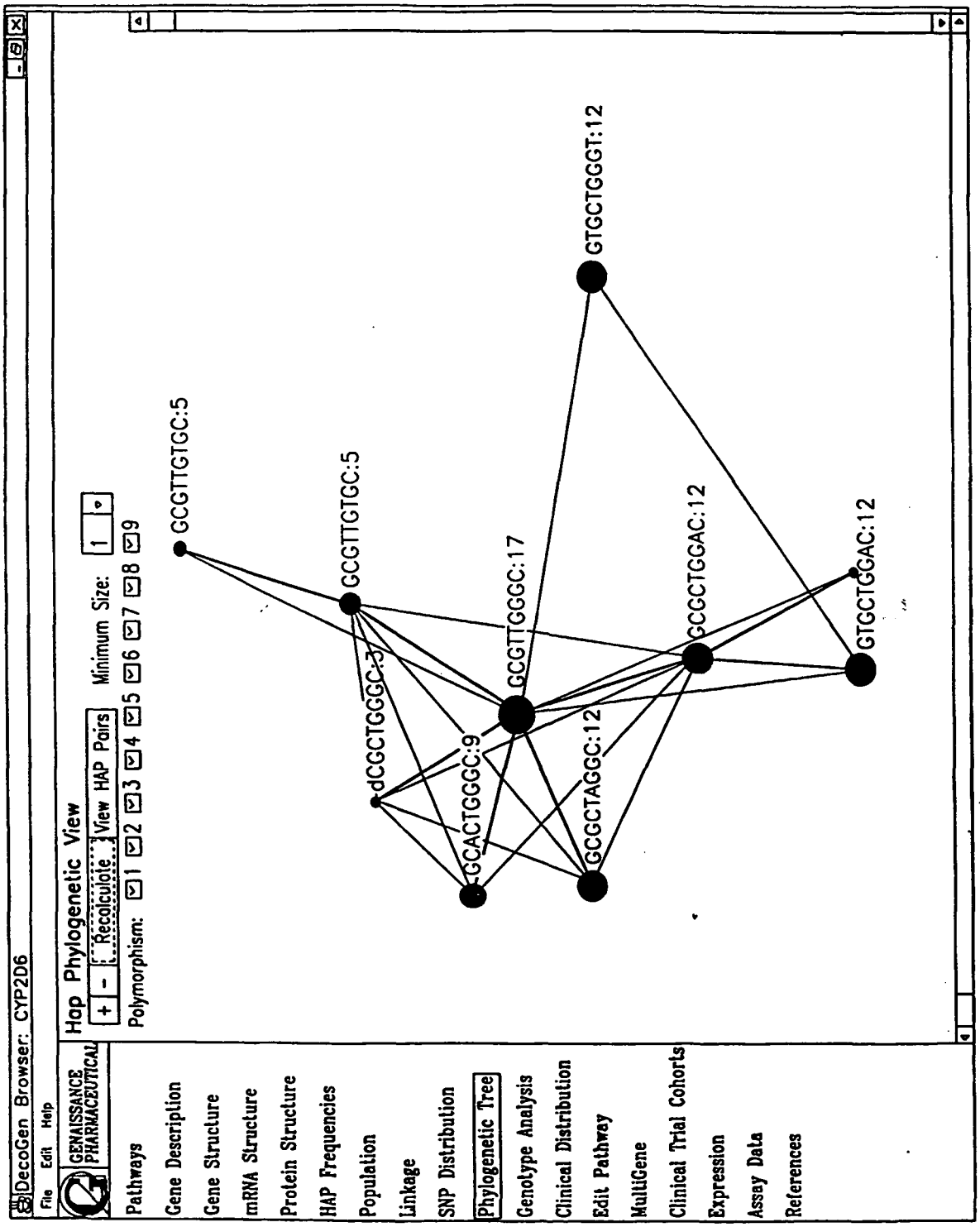

DecoGen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Hap Phylogenetic View
+ - Recalculate View HAP Pairs
Minimum Size: 1
Polymorphism: 1 2 3 4 5 6 7 8 9
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References
GCGTTGTGC:5
GCGTTGTGC:5
dCCCTGGGC:3
GCACTGGGC:9
GCGTTGGGC:17
GCGCTAGGC:12
GTGCTGGGT:12
GCGCTGGAC:12
GTGCTGGAC:12

FIG. 18

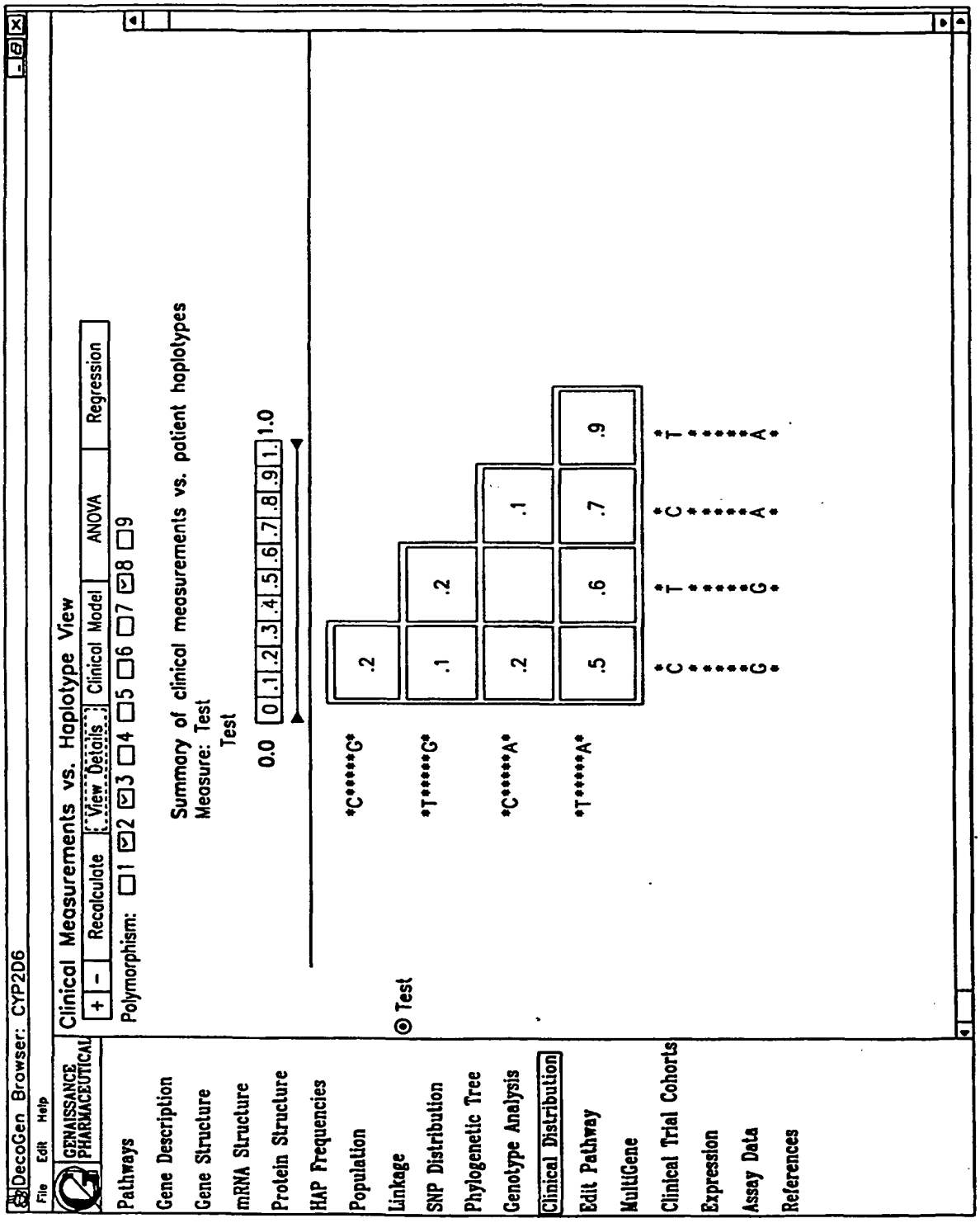
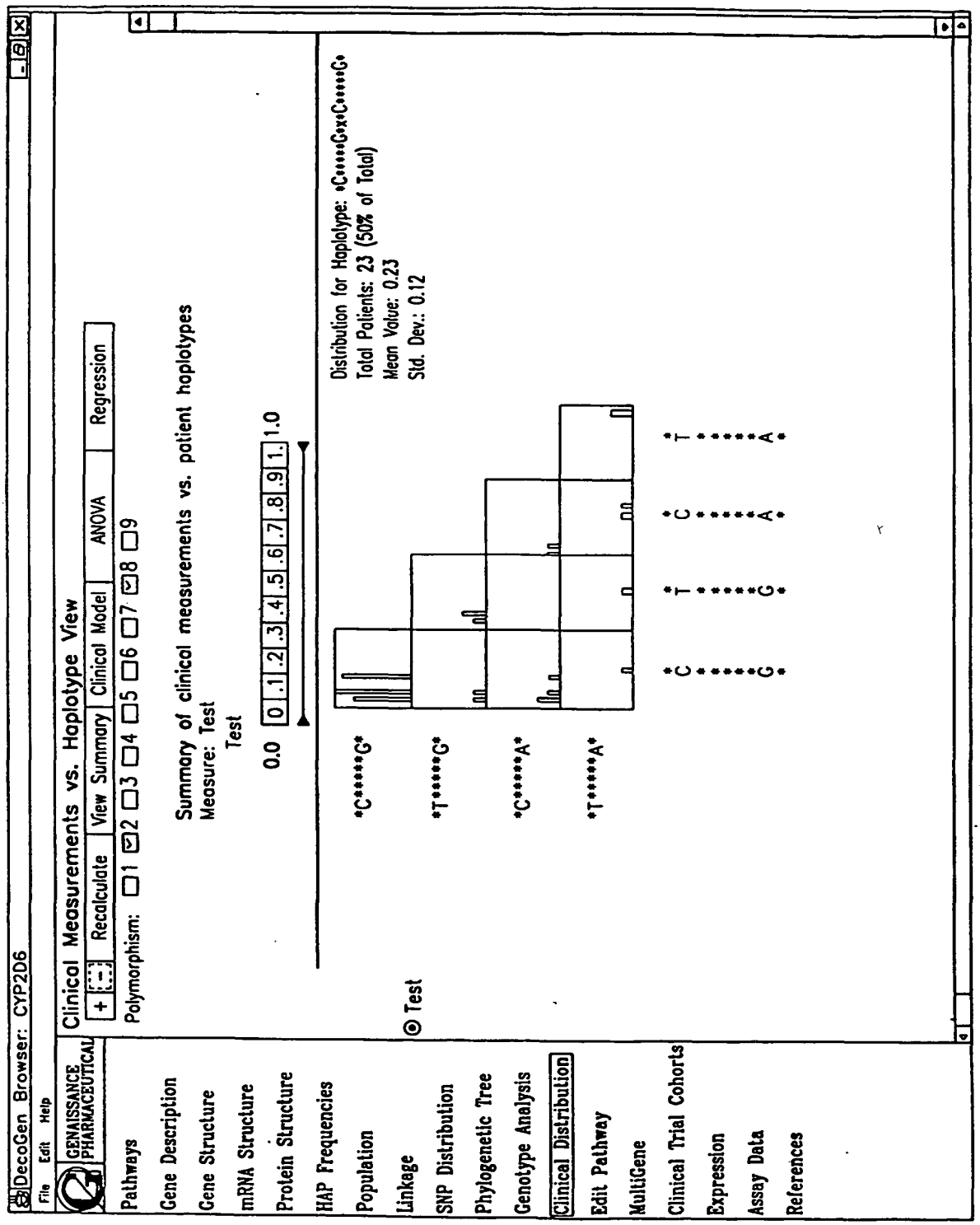

DecoGen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Clinical Measurements vs. Haplotype View
+ - Recalculate View Details Clinical Model ANOVA Regression
Polymorphism: 1 2 3 4 5 6 7 8 9
Summary of clinical measurements vs. patient haplotypes
Measure: Test
Test
0.0 0 .1 .2 .3 .4 .5 .6 .7 .8 .9 1. 1.0
Test
*C*****C*
*T*****C*
*C*****A*
*T*****A*
.2
.1 .2
.2 .1
.5 .6 .7 .9
*C*****C*
*C*****G*
*T*****C*
*T*****G*
*C*****A*
*T*****A*
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References

FIG. 19


DecoGen Browser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Clinicol Measurements vs. Haplotype View
+ Recalculate View Summary Clinical Model ANOVA Regression
Polymorphism: 1 2 3 4 5 6 7 8 9
Summary of clinical measurements vs. patient haplotypes
Measure: Test
Test
0.0 0 .1 .2 .3 .4 .5 .6 .7 .8 .9 1. 1.0
Distribution for Haplotype: *C*****G*C*****G*
Total Patients: 23 (50% of Total)
Mean Value: 0.23
Std. Dev.: 0.12
Test
*C*****G*
*T*****G*
*C*****A*
*T*****A*
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References

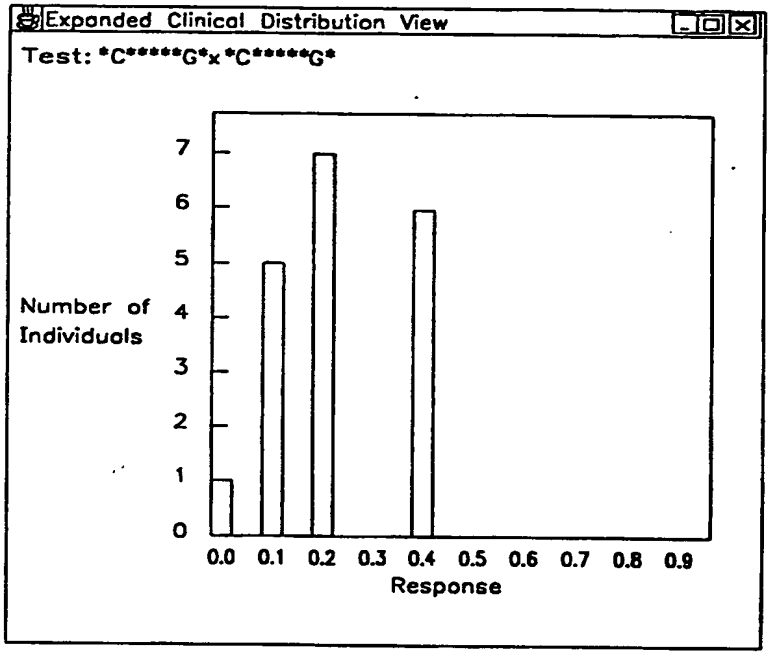
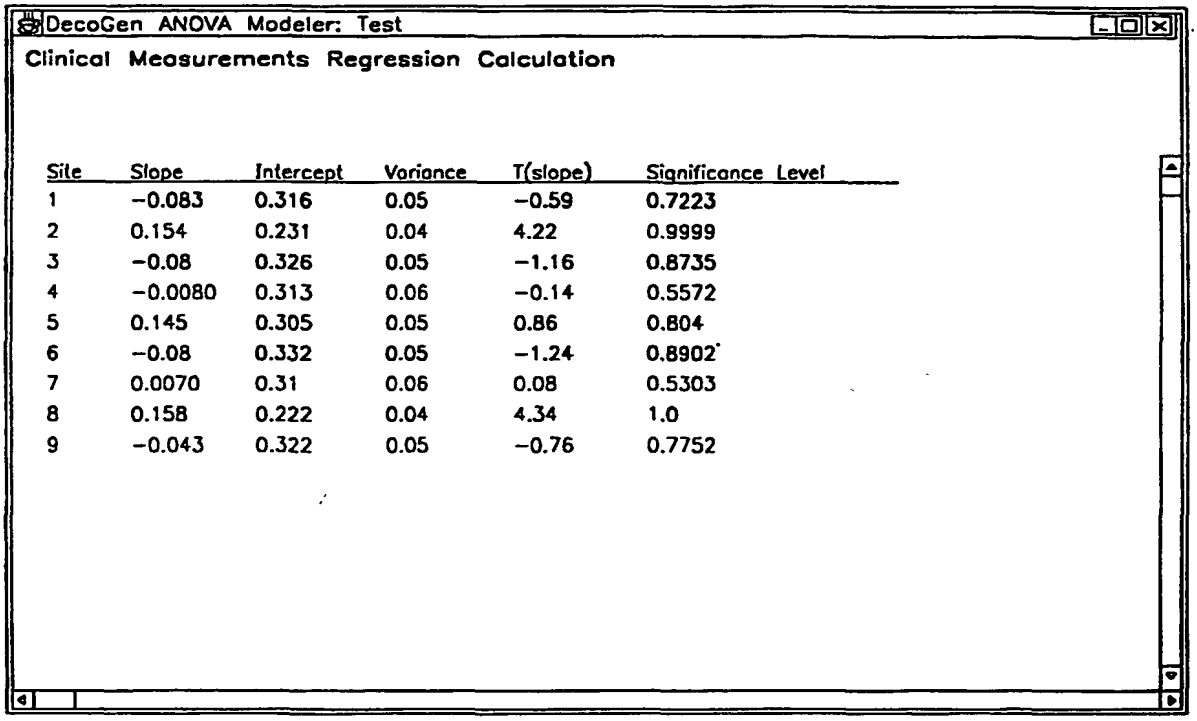

Expanded Clinical Distribution View
Test: *C*****G*x*C*****G*
Number of Individuals
0
1
2
3
4
5
6
7
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9
Response

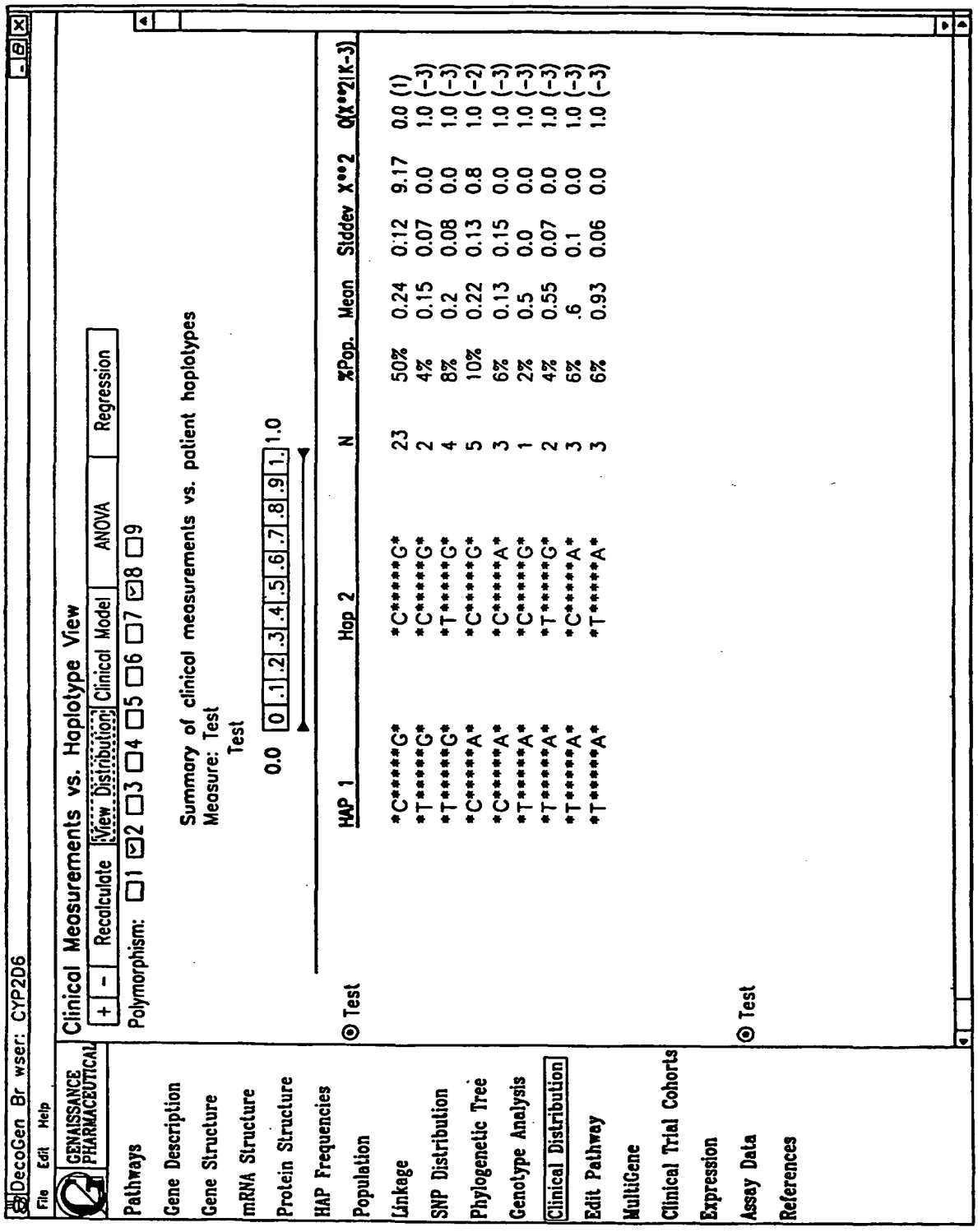
FIG. 20



Site	Slope	Intercept	Variance	T(slope)	Significance Level
1	−0.083	0.316	0.05	−0.59	0.7223
2	0.154	0.231	0.04	4.22	0.9999
3	−0.08	0.326	0.05	−1.16	0.8735
4	−0.0080	0.313	0.06	−0.14	0.5572
5	0.145	0.305	0.05	0.86	0.804
6	−0.08	0.332	0.05	−1.24	0.8902
7	0.0070	0.31	0.06	0.08	0.5303
8	0.158	0.222	0.04	4.34	1.0
9	−0.043	0.322	0.05	−0.76	0.7752

FIG. 21

FIG. 22


DecoGen Br wser: CYP2D6
File Edit Help
GENAISSANCE PHARMACEUTICALS
Clinical Measurements vs. Haplotype View
+ - Recalculate View Distribution Clinical Model ANOVA Regression
Polymorphism: 1 2 3 4 5 6 7 8 9
Pathways
Gene Description
Gene Structure
mRNA Structure
Protein Structure
HAP Frequencies
Population
Linkage
SNP Distribution
Phylogenetic Tree
Genotype Analysis
Clinical Distribution
Edit Pathway
MultiGene
Clinical Trial Cohorts
Expression
Assay Data
References
Summary of clinical measurements vs. patient haplotypes
Measure: Test
Test
0.0 0 .1 .2 .3 .4 .5 .6 .7 .8 .9 1. 1.0
Test
HAP 1 Hap 2 N %Pop. Mean Stddev X**2 Q(X**2|K-3)
*C*****G* *C*****G* 23 50% 0.24 0.12 9.17 0.0 (1)
*T*****G* *C*****G* 2 4% 0.15 0.07 0.0 1.0 (-3)
*T*****G* *T*****G* 4 8% 0.2 0.08 0.0 1.0 (-3)
*C*****A* *C*****G* 5 10% 0.22 0.13 0.8 1.0 (-2)
*C*****A* *C*****A* 3 6% 0.13 0.15 0.0 1.0 (-3)
*T*****A* *C*****G* 1 2% 0.5 0.0 0.0 1.0 (-3)
*T*****A* *T*****G* 2 4% 0.55 0.07 0.0 1.0 (-3)
*T*****A* *C*****A* 3 6% .6 0.1 0.0 1.0 (-3)
*T*****A* *T*****A* 3 6% 0.93 0.06 0.0 1.0 (-3)
Test

Dec Gen ANOVA Modeler: Test

Clinical Measurements ANOVA Calculation

+ − Recalculate

Polymorphism: ☐1 ☑2 ☐3 ☐4 ☐5 ☐6 ☐7 ☑8 ☐9

Source of Variation	DF	Mean Squares	F-ratio
Between Groups	7	0.26	19.65
Within Groups	37	0.01	

Critical F-Distribution Value 90%: 1.88
Critical F-Distribution Value 95%: 2.26
Critical F-Distribution Value 99%: 3.16

Significant between-group variation at the 90% cofidence level
Significant between-group variation at the 95% confidence level
Significant between-group variation at the 99% confidence level

HAP 1	HAP 2	N	Average	Std. Dev.
*C*****G*	*C*****G*	23	0.23	0.12
*C*****G*	*T*****G*	2	0.15	0.07
*C*****G*	*C*****A*	5	0.22	0.13
*T*****G*	*T*****G*	4	0.2	0.08
*T*****G*	*T*****A*	2	0.55	0.07
*C*****A*	*C*****A*	3	0.13	0.15
*C*****A*	*T*****A*	3	0.6	0.09
*T*****A*	*T*****A*	3	0.93	0.05

FIG. 23

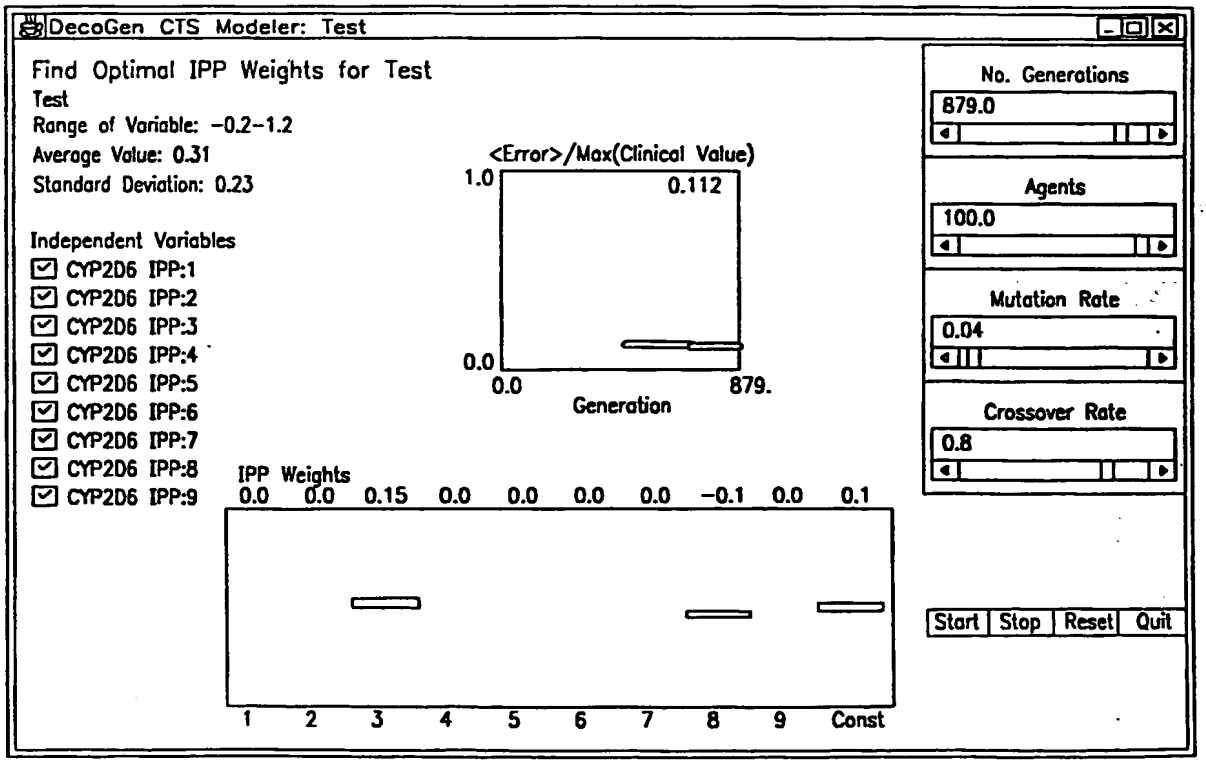


FIG. 24

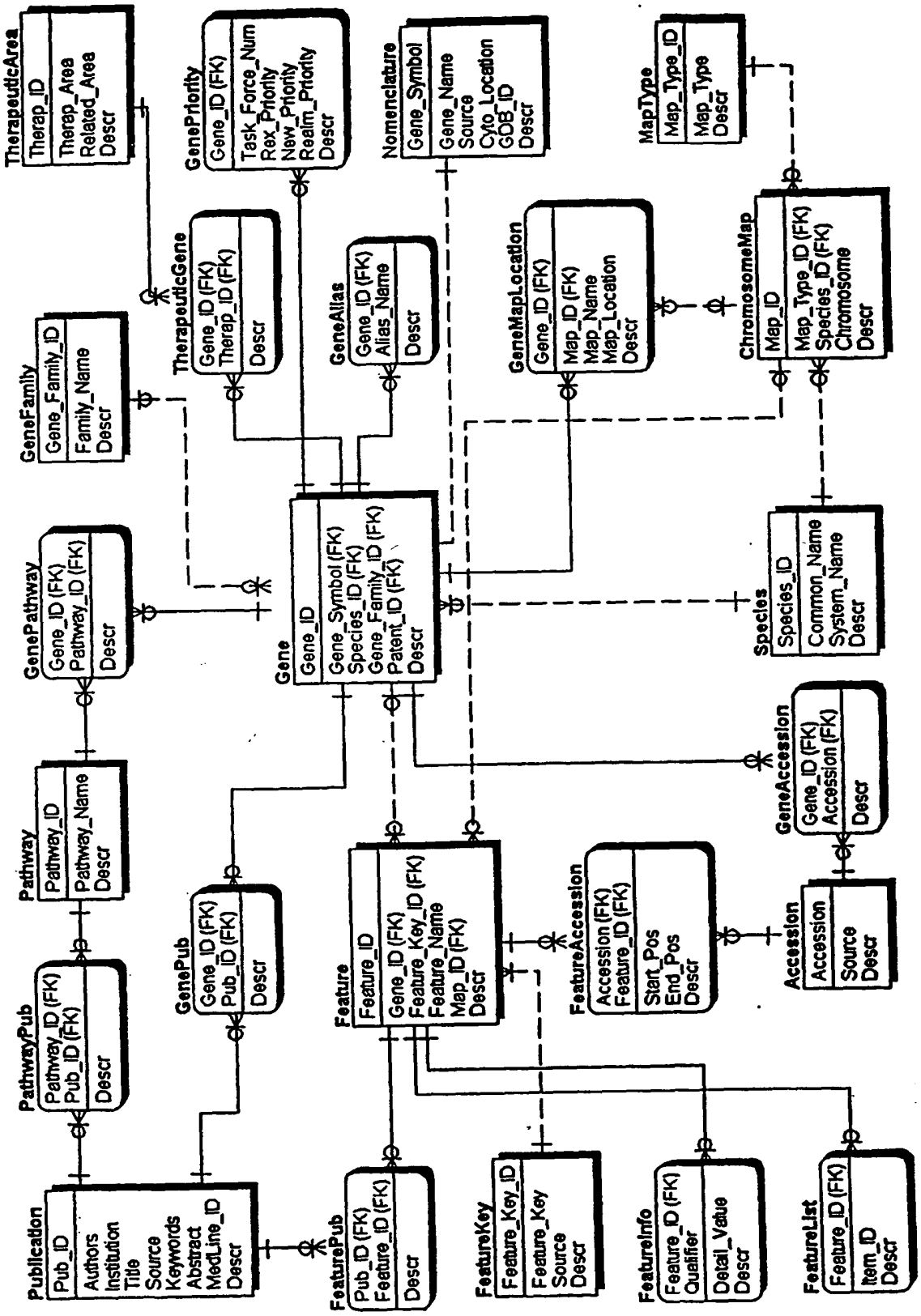
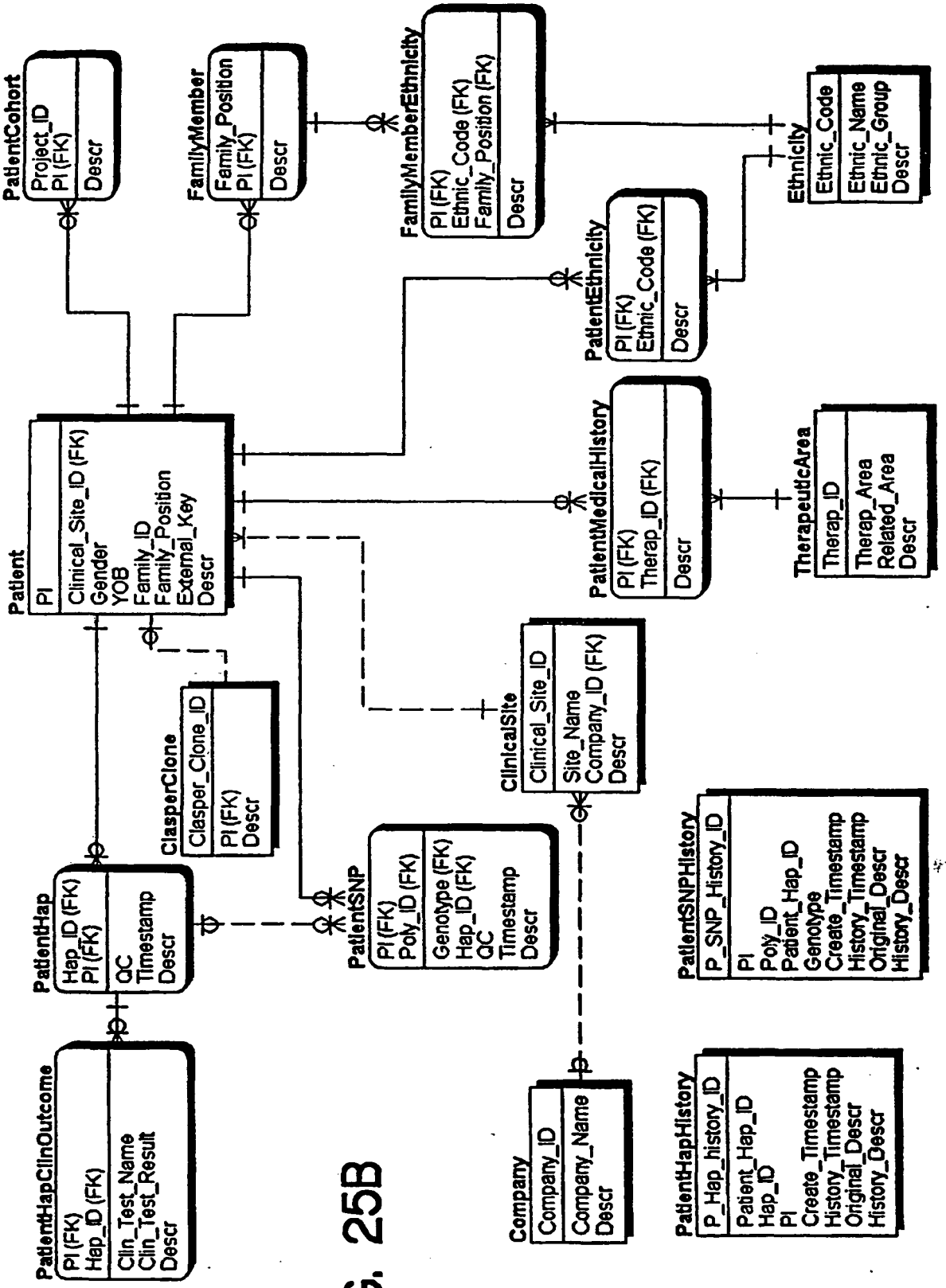

TherapeuticArea
Therap_ID
Therap_Area
Related_Area
Descr
GenePriority
Gene_ID (FK)
Task_Force_Num
Rex_Priority
New_Priority
Realm_Priority
Descr
Nomenclature
Gene_Symbol
Gene_Name
Source
Cyto_Location
GDB_ID
Descr
MapType
Map_Type_ID
Map_Type
Descr
TherapeuticGene
Gene_ID (FK)
Therap_ID (FK)
Descr
GeneAlias
Gene_ID (FK)
Alias_Name
Descr
GeneMapLocation
Gene_ID (FK)
Map_ID (FK)
Map_Name
Map_Location
Descr
ChromosomeMap
Map_ID
Map_Type_ID (FK)
Species_ID (FK)
Chromosome
Descr
GeneFamily
Gene_Family_ID
Family_Name
Descr
GenePathway
Gene_ID (FK)
Pathway_ID (FK)
Descr
Gene
Gene_ID
Gene_Symbol (FK)
Species_ID (FK)
Gene_Family_ID (FK)
Patent_ID (FK)
Descr
Species
Species_ID
Common_Name
System_Name
Descr
GeneAccession
Gene_ID (FK)
Accession (FK)
Descr
Pathway
Pathway_ID
Pathway_Name
Descr
GenePub
Gene_ID (FK)
Pub_ID (FK)
Descr
Feature
Feature_ID
Gene_ID (FK)
Feature_Key_ID (FK)
Feature_Name
Map_ID (FK)
Descr
FeatureAccession
Accession (FK)
Feature_ID (FK)
Start_Pos
End_Pos
Descr
Accession
Accession
Source
Descr
PathwayPub
Pathway_ID (FK)
Pub_ID (FK)
Descr
Publication
Pub_ID
Authors
Institution
Title
Source
Keywords
Abstract
MedLine_ID
Descr
FeaturePub
Pub_ID (FK)
Feature_ID (FK)
Descr
FeatureKey
Feature_Key_ID
Feature_Key
Source
Descr
FeatureInfo
Feature_ID (FK)
Qualifier
Detail_Value
Descr
FeatureList
Feature_ID (FK)
Item_ID
Descr

FIG. 25A


PatientCohort
Project_ID
PI (FK)
Descr
FamilyMember
Family_Position
PI (FK)
Descr
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Family_Position (FK)
Descr
Ethnicity
Ethnic_Code
Ethnic_Name
Ethnic_Group
Descr
PatientEthnicity
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Ethnic_Code (FK)
Descr
Patient
PI
Clinical_Site_ID (FK)
Gender
YOB
Family_ID
Family_Position
External_Key
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PatientMedicalHistory
PI (FK)
Therap_ID (FK)
Descr
TherapeuticArea
Therap_ID
Therap_Area
Related_Area
Descr
ClinicalSite
Clinical_Site_ID
Site_Name
Company_ID (FK)
Descr
ClasperClone
Clasper_Clone_ID
PI (FK)
Descr
PatientHap
Hap_ID (FK)
PI (FK)
QC
Timestamp
Descr
PatientSNP
PI (FK)
Poly_ID (FK)
Genotype (FK)
Hap_ID (FK)
QC
Timestamp
Descr
PatientSNPHistory
P_SNP_History_ID
PI
Poly_ID
Patient_Hap_ID
Genotype
Create_Timestamp
History_Timestamp
Original_Descr
History_Descr
PatientHapClinOutcome
PI (FK)
Hap_ID (FK)
Clin_Test_Name
Clin_Test_Result
Descr
Company
Company_ID
Company_Name
Descr
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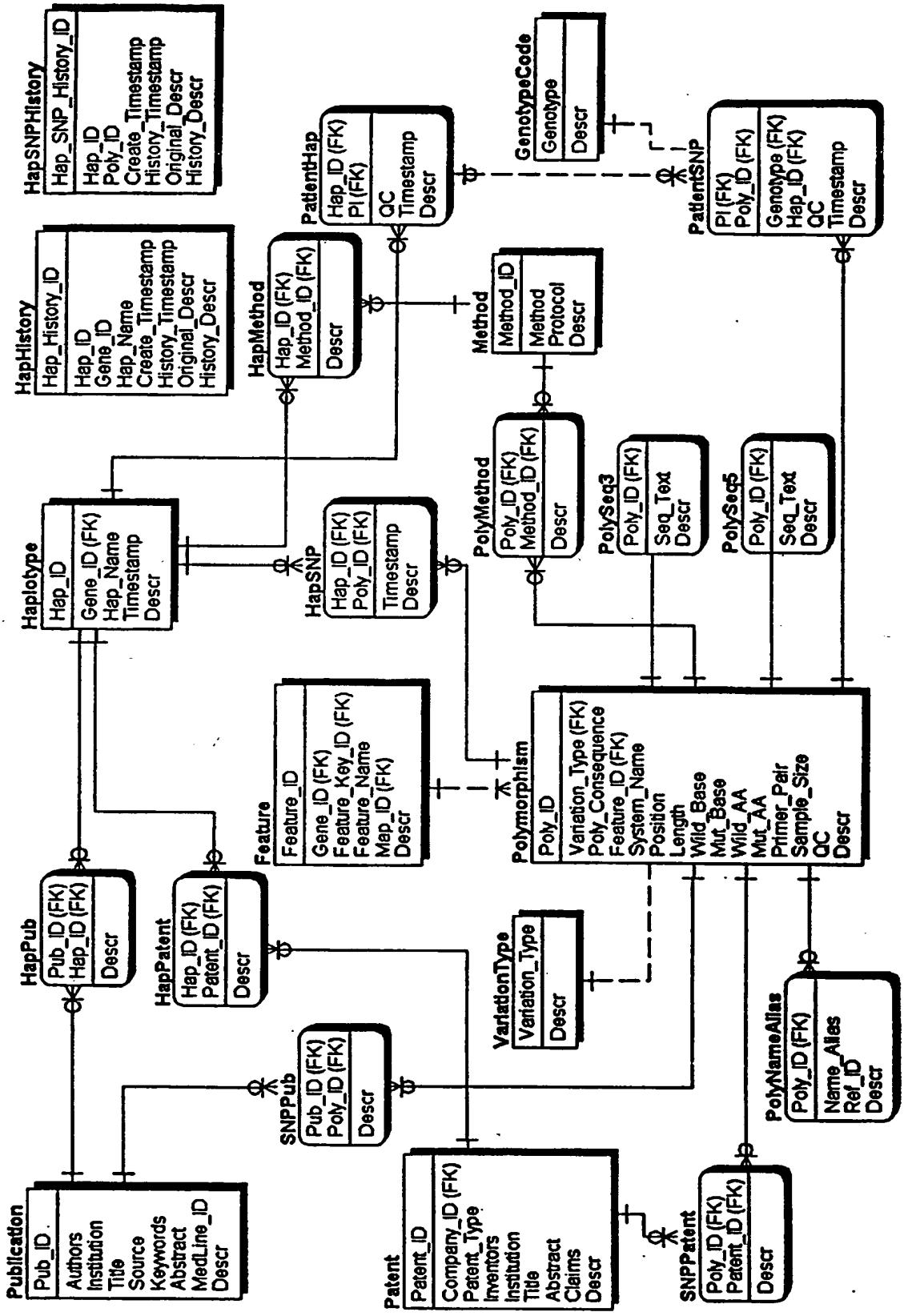
P_Hap_history_ID
Patient_Hap_ID
Hap_ID
PI
Create_Timestamp
History_Timestamp
Original_Descr
History_Descr

FIG. 25B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Hap_SNP_History_ID
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Poly_ID
Create_Timestamp
History_Timestamp
Original_Descr
History_Descr
HapHistory
Hap_History_ID
Hap_ID
Gene_ID
Hap_Name
Create_Timestamp
History_Timestamp
Original_Descr
History_Descr
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PI (FK)
QC
Timestamp
Descr
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Genotype
Descr
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Genotype (FK)
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QC
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Method_ID (FK)
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Method
Method_ID
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Poly_ID (FK)
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Polymorphism
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Poly_Consequence
Feature_ID (FK)
System_Name
Position
Length
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Mut_Base
Wild_AA
Mut_AA
Primer_Pair
Sample_Size
QC
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Hap_ID (FK)
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Patent_ID (FK)
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VariationType
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Descr
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Ref_ID
Descr
Publication
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Authors
Institution
Title
Source
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Company_ID (FK)
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Inventors
Institution
Title
Abstract
Claims
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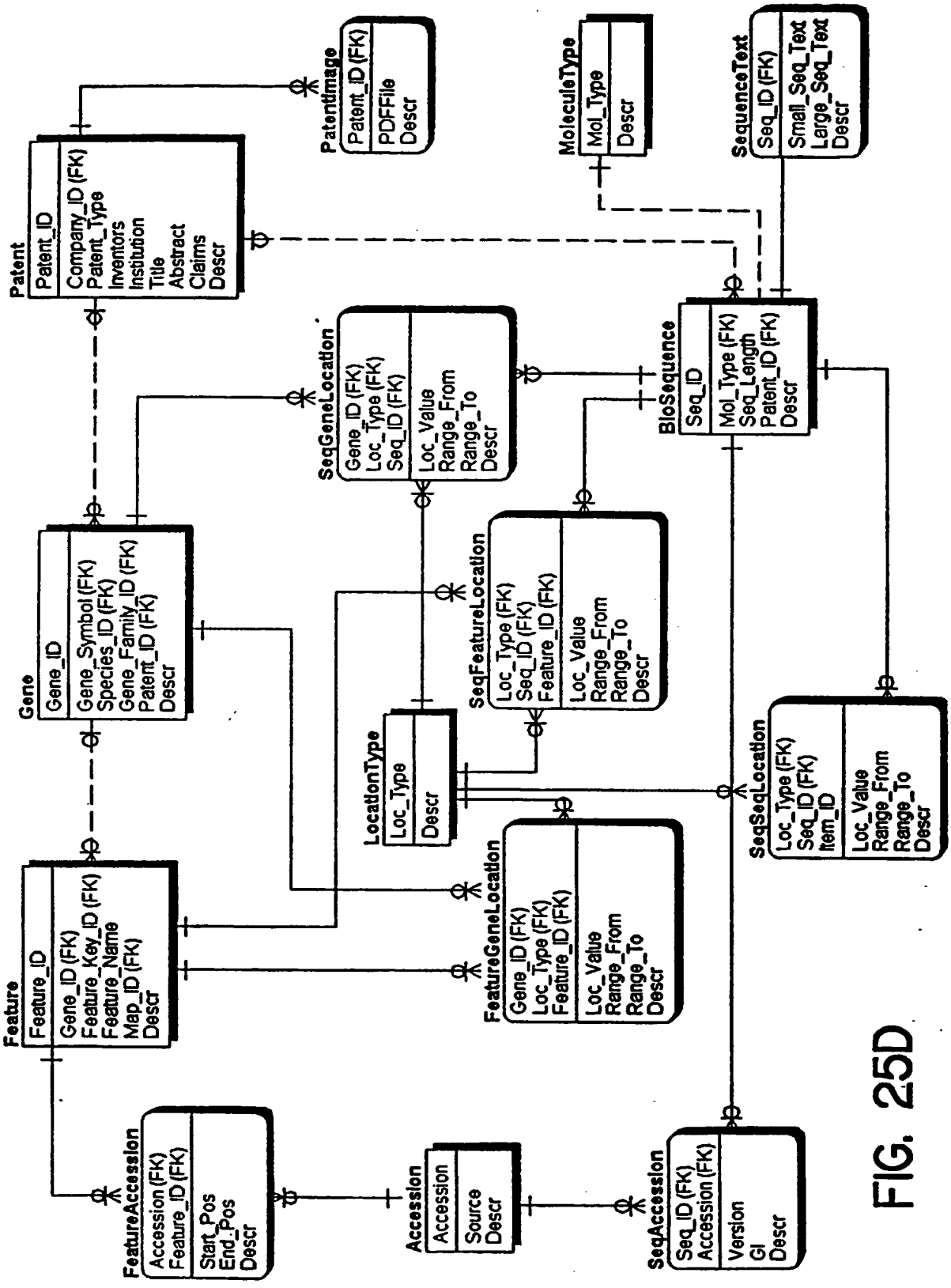
Poly_ID (FK)
Patent_ID (FK)
Descr

FIG. 25C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Mol_Type
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Small_Seq_Text
Large_Seq_Text
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Company_ID (FK)
Patent_Type
Inventors
Institution
Title
Abstract
Claims
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Loc_Type (FK)
Seq_ID (FK)
Loc_Value
Range_From
Range_To
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BioSequence
Seq_ID
Mol_Type (FK)
Seq_Length
Patent_ID (FK)
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Gene_Symbol (FK)
Species_ID (FK)
Gene_Family_ID (FK)
Patent_ID (FK)
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Range_From
Range_To
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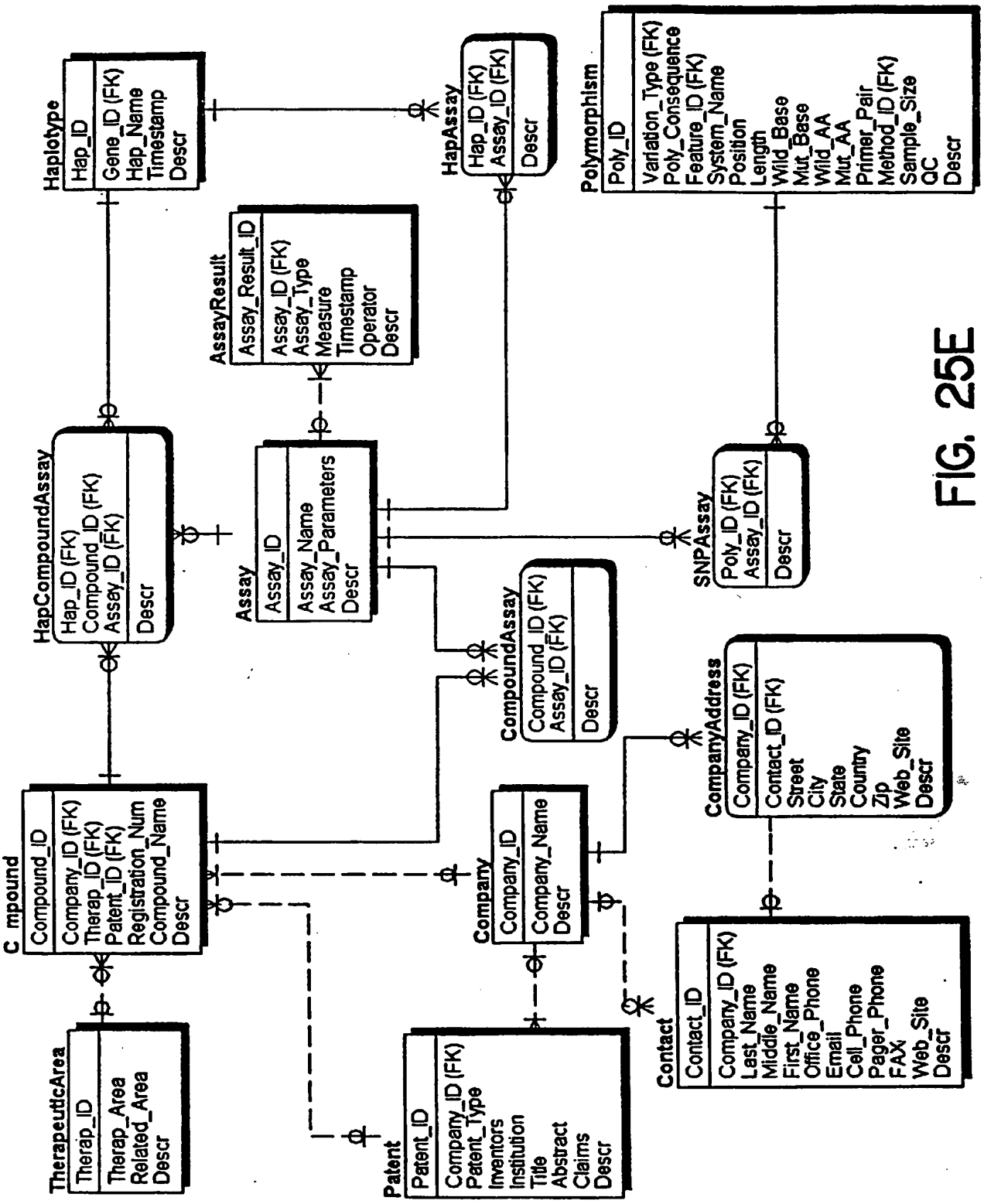
LocationType
Loc_Type
Descr
SeqSeqLocation
Loc_Type (FK)
Seq_ID (FK)
Item_ID
Loc_Value
Range_From
Range_To
Descr
Feature
Feature_ID
Gene_ID (FK)
Feature_Key_ID (FK)
Feature_Name
Map_ID (FK)
Descr
FeatureGeneLocation
Gene_ID (FK)
Loc_Type (FK)
Feature_ID (FK)
Loc_Value
Range_From
Range_To
Descr
FeatureAccession
Accession (FK)
Feature_ID (FK)
Start_Pos
End_Pos
Descr
Accession
Accession
Source
Descr
SeqAccession
Seq_ID (FK)
Accession (FK)
Version
GI
Descr

FIG. 25D


Haplotype
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Gene_ID (FK)
Hap_Name
Timestamp
Descr
HapAssay
Hap_ID (FK)
Assay_ID (FK)
Descr
Polymorphism
Poly_ID
Variation_Type (FK)
Poly_Consequence
Feature_ID (FK)
System_Name
Position
Length
Wild_Base
Mut_Base
Wild_AA
Mut_AA
Primer_Pair
Method_ID (FK)
Sample_Size
QC
Descr
AssayResult
Assay_Result_ID
Assay_ID (FK)
Assay_Type
Measure
Timestamp
Operator
Descr
HapCompoundAssay
Hap_ID (FK)
Compound_ID (FK)
Assay_ID (FK)
Descr
Assay
Assay_ID
Assay_Name
Assay_Parameters
Descr
SNPAssay
Poly_ID (FK)
Assay_ID (FK)
Descr
CompoundAssay
Compound_ID (FK)
Assay_ID (FK)
Descr
CompanyAddress
Company_ID (FK)
Contact_ID (FK)
Street
City
State
Country
Zip
Web_Site
Descr
Compound
Compound_ID
Company_ID (FK)
Therap_ID (FK)
Patent_ID (FK)
Registration_Num
Compound_Name
Descr
Company
Company_ID
Company_Name
Descr
Contact
Contact_ID
Company_ID (FK)
Last_Name
Middle_Name
First_Name
Office_Phone
Email
Cell_Phone
Pager_Phone
FAX
Web_Site
Descr
TherapeuticArea
Therap_ID
Therap_Area
Related_Area
Descr
Patent
Patent_ID
Company_ID (FK)
Patent_Type
Inventors
Institution
Title
Abstract
Claims
Descr

FIG. 25E

Legend of Figures:

Rectangle Boxes: Tables in the database.

Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

2: Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.

4: Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.

6: Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.

8: Non-identifying parent / child relationship. It represents the not nullable 1-to-1-or-many relationship.

10: Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.

12: Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-exact-1 relationship.

14: Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.

FIG. 25F

FIG. 26

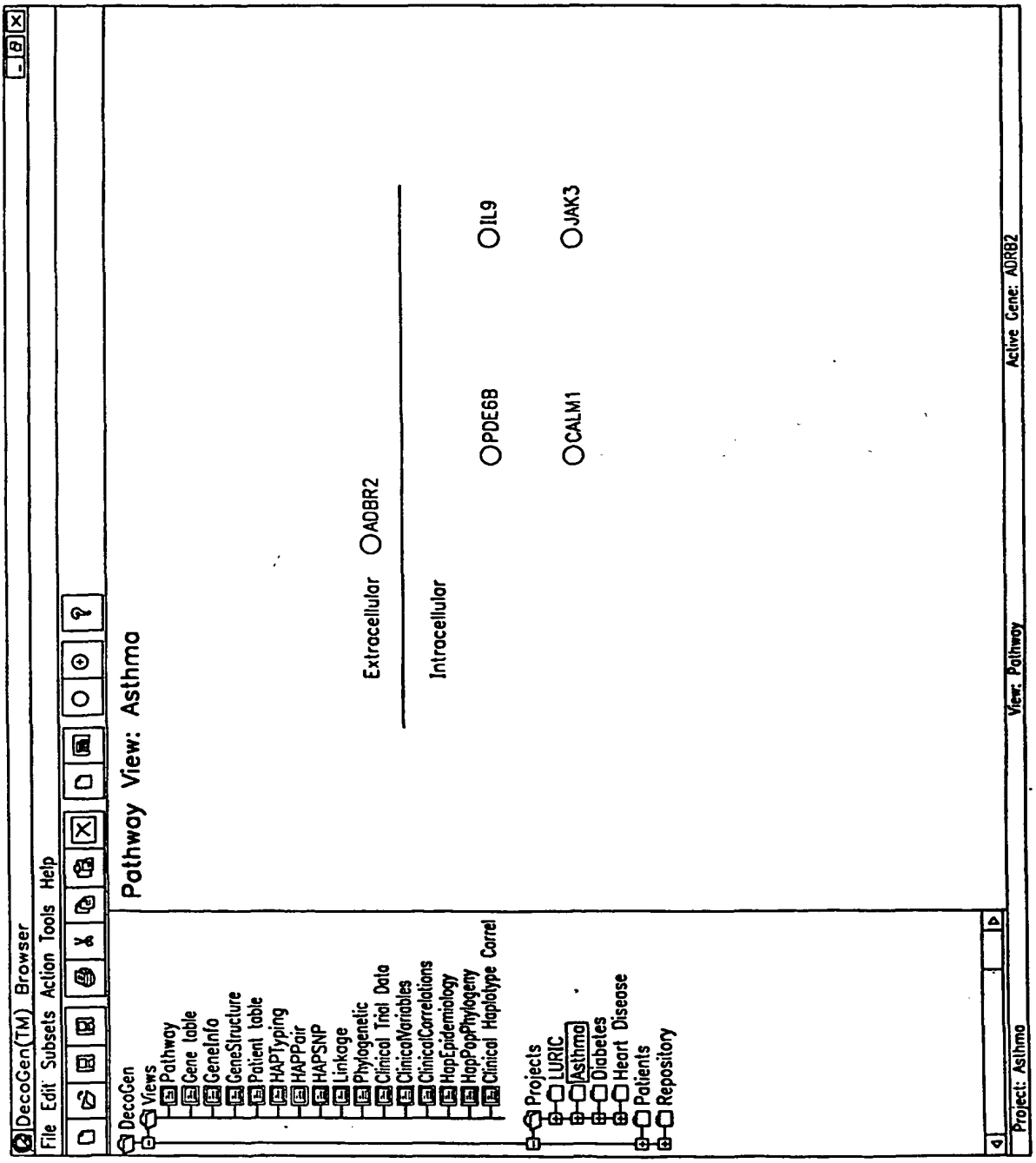

DecoGen(TM) Browser
File Edit Subsets Action Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Patients
Repository
Pathway View: Asthma
Extracellular
ADBR2
Intracellular
PDE6B
IL9
CALM1
JAK3
Project: Asthma
View: Pathway
Active Gene: ADRB2

FIG. 27

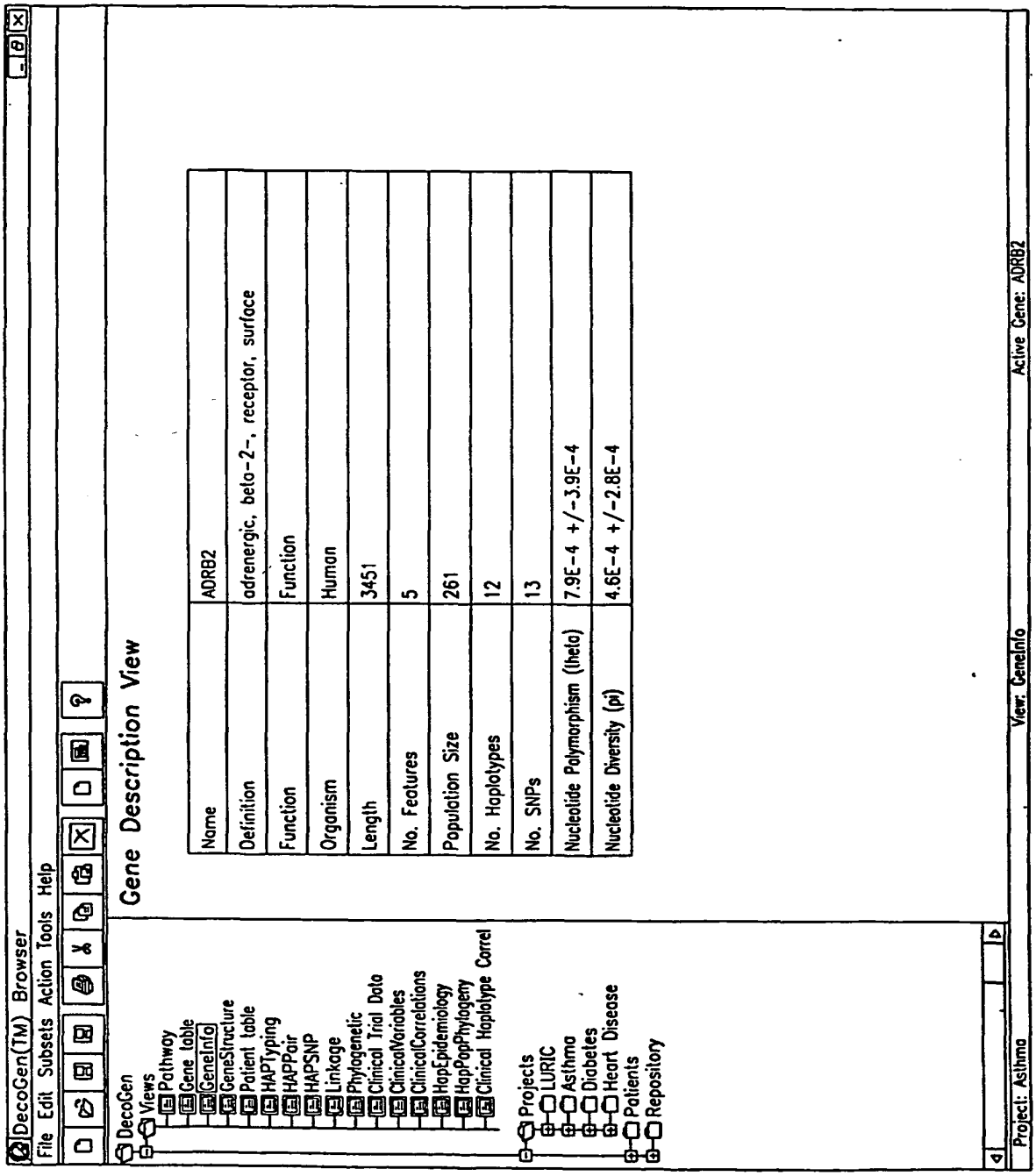
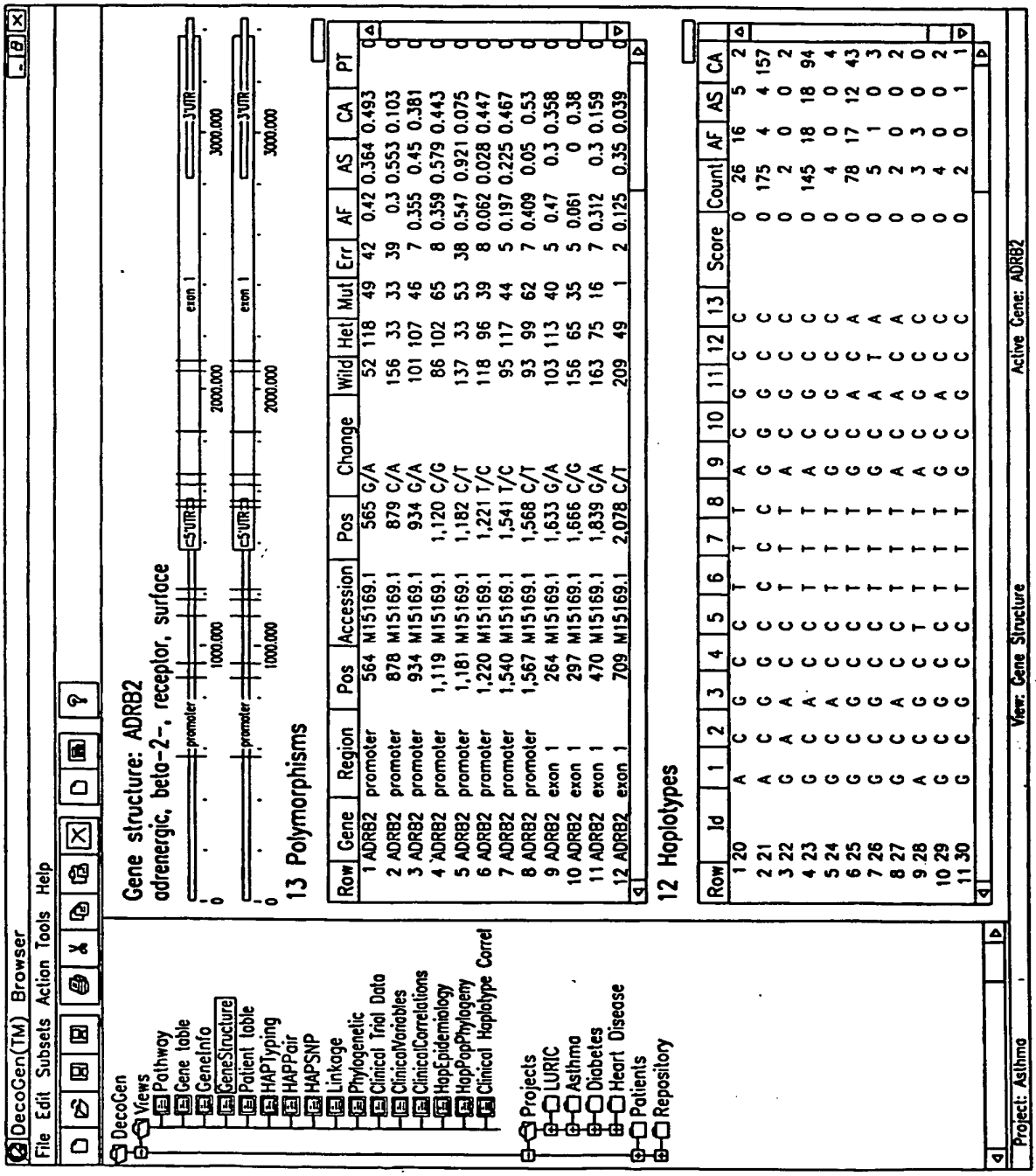

DecoGen(TM) Browser
File Edit Subsets Action Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Patients
Repository
Gene Description View
Name ADRB2
Definition adrenergic, beta-2-, receptor, surface
Function Function
Organism Human
Length 3451
No. Features 5
Population Size 261
No. Haplotypes 12
No. SNPs 13
Nucleotide Polymorphism (theta) 7.9E-4 +/-3.9E-4
Nucleotide Diversity (pi) 4.6E-4 +/-2.8E-4
Project: Asthma
View: GeneInfo
Active Gene: ADRB2

FIG. 28A



SUBSTITUTE SHEET (RULE 26)

FIG. 28B

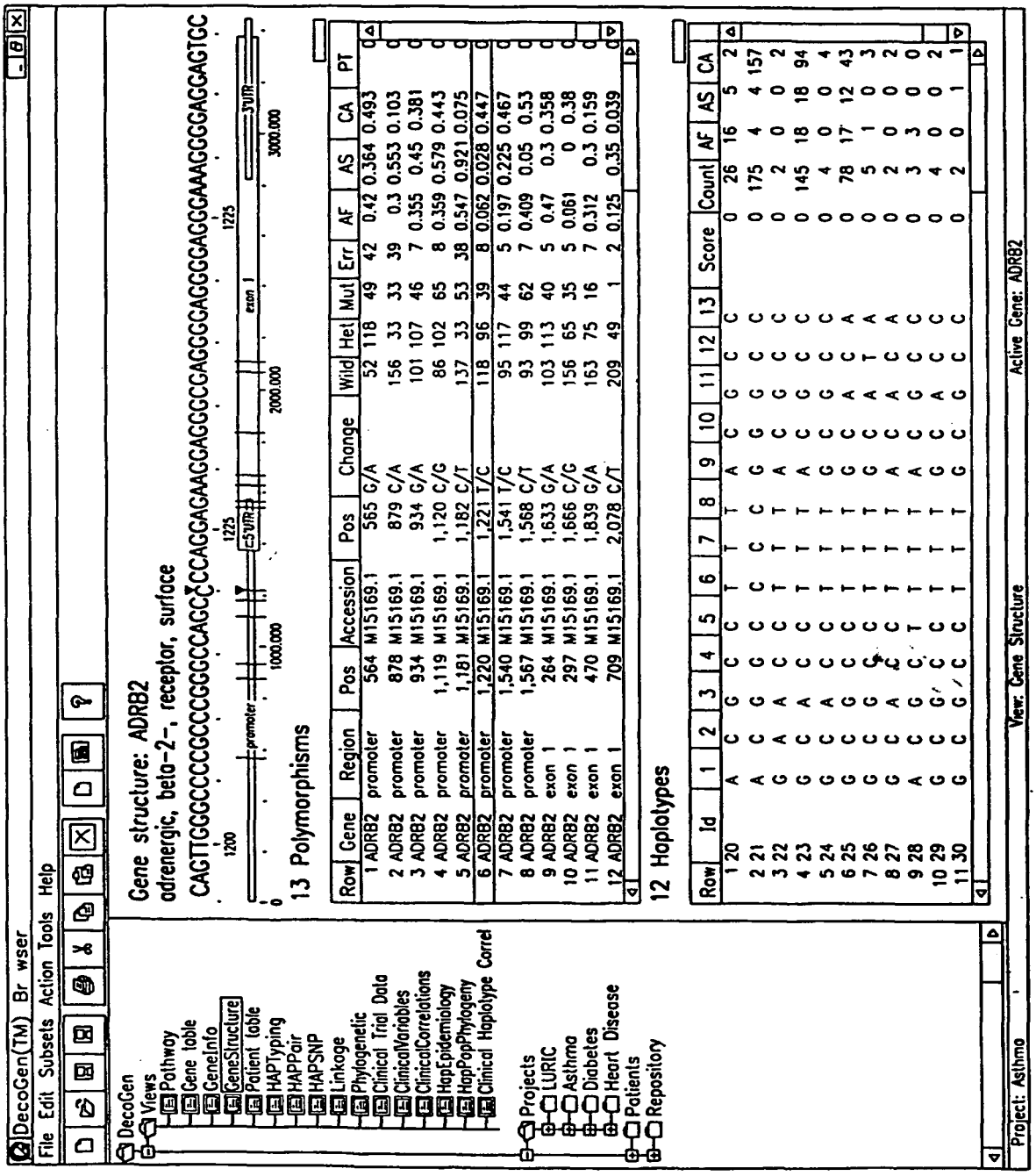

DecoGen(TM) Br wser
File Edit Subsets Action Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Patients
Repository
Gene structure: ADRB2
adrenergic, beta-2-, receptor, surface
CAGTTGGCCCCCGCCCGGGCCAGCCCCAGGAGAAGGAGGGCCAGGGGAGGGAAGGGGAGGAGTGC
1200
1225
promoter
5'UTR
exon 1
3'UTR
1000.000
2000.000
3000.000
13 Polymorphisms
Row Gene Region Pos Accession Pos Change Wild Het Mut Err AF AS CA PT
1 ADRB2 promoter 564 M15169.1 565 C/A 52 118 49 42 0.42 0.364 0.493
2 ADRB2 promoter 878 M15169.1 879 C/A 156 33 33 39 0.3 0.553 0.103
3 ADRB2 promoter 934 M15169.1 934 G/A 101 107 46 7 0.355 0.45 0.381
4 ADRB2 promoter 1,119 M15169.1 1,120 C/G 86 102 65 8 0.359 0.579 0.443
5 ADRB2 promoter 1,181 M15169.1 1,182 C/T 137 33 53 38 0.547 0.921 0.075
6 ADRB2 promoter 1,220 M15169.1 1,221 T/C 118 96 39 8 0.062 0.028 0.447
7 ADRB2 promoter 1,540 M15169.1 1,541 T/C 95 117 44 5 0.197 0.225 0.467
8 ADRB2 promoter 1,567 M15169.1 1,568 C/T 93 99 62 7 0.409 0.05 0.53
9 ADRB2 exon 1 264 M15169.1 1,633 G/A 103 113 40 5 0.47 0.3 0.358
10 ADRB2 exon 1 297 M15169.1 1,666 C/G 156 65 35 5 0.061 0 0.38
11 ADRB2 exon 1 470 M15169.1 1,839 G/A 163 75 16 7 0.312 0.3 0.159
12 ADRB2 exon 1 709 M15169.1 2,078 C/T 209 49 1 2 0.125 0.35 0.039
12 Haplotypes
Row Id 1 2 3 4 5 6 7 8 9 10 11 12 13 Score Count AF AS CA
1 20 A C G C C C T T T A C G C C 0 26 16 5 2
2 21 A C G G C C C C C G G G C C 0 175 4 4 157
3 22 G A A C C C T T T A C G C C 0 2 0 0 2
4 23 G C A C C C T T T A C G C C 0 145 18 18 94
5 24 G C A C C C T T T G C G C C 0 4 0 0 4
6 25 G C G C C C T T T G C A C A 0 78 17 12 43
7 26 G C G C C C T T T G C A T A 0 5 1 0 3
8 27 G C A C C C T T T A C A C A 0 2 0 0 2
9 28 A C G C C T T T T A C G C C 0 3 3 0 0
10 29 G C G C C C T T T G C A C C 0 4 0 0 2
11 30 G C G C C C T T T G C G C C 0 2 0 1 1
Project: Asthma
View: Gene Structure
Active Gene: ADRB2

FIG. 29A

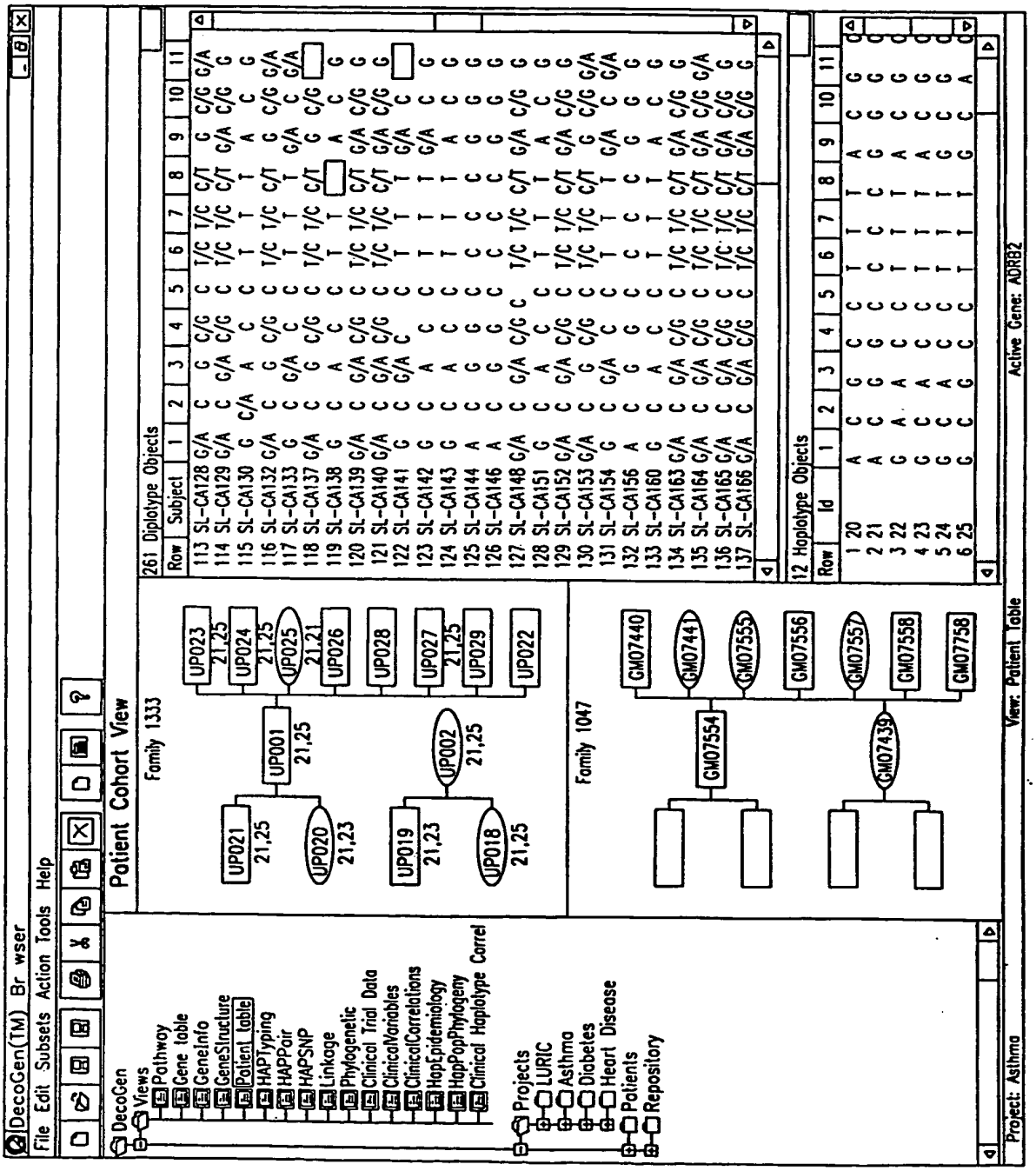
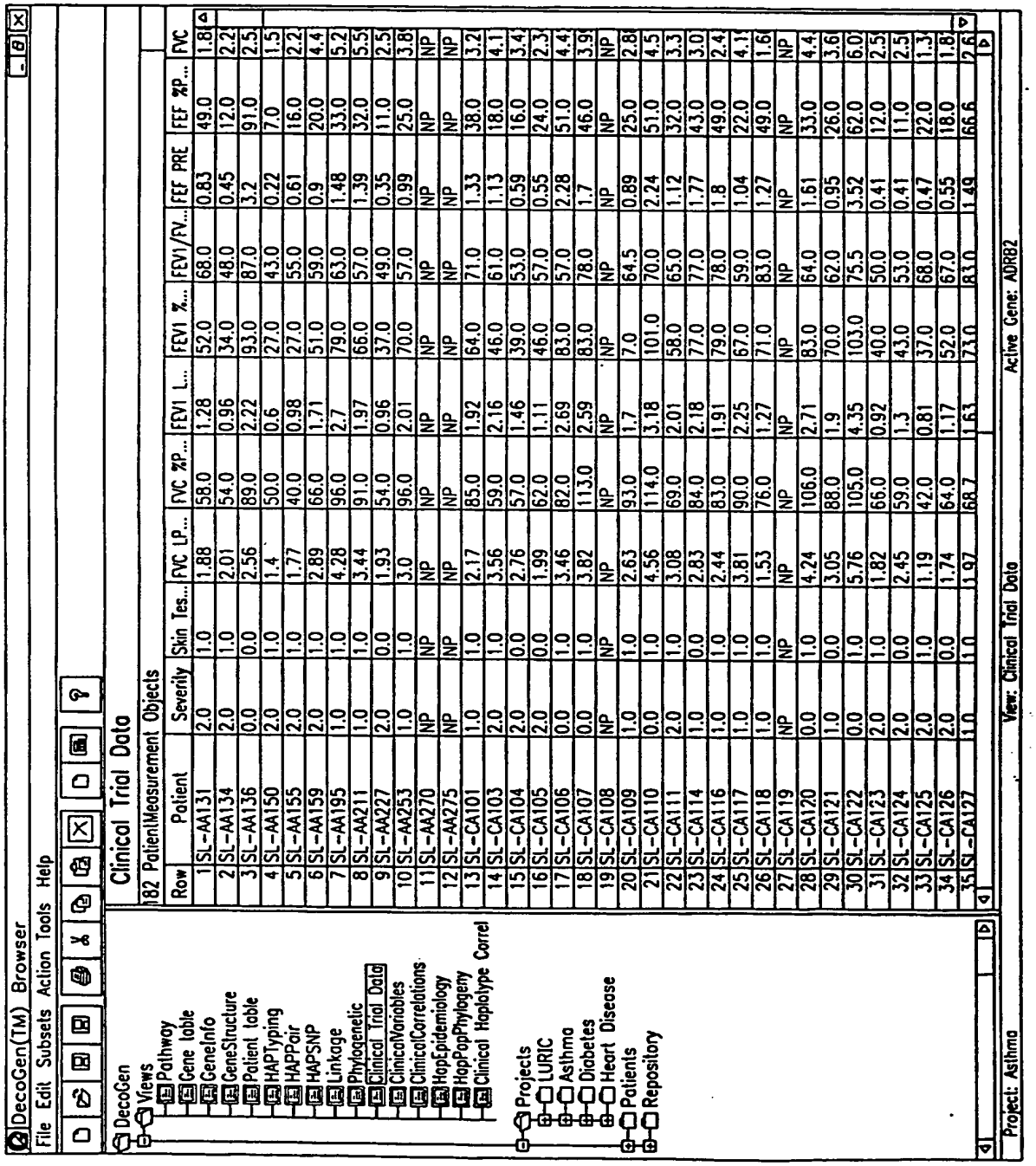

DecoGen(TM) Br wser
File Edit Subsets Action Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Patients
Repository
Patient Cohort View
Family 1333
UP023 21,25
UP024 21,25
UP025 21,21
UP026
UP028
UP027 21,25
UP029
UP022
UP001 21,25
UP002 21,25
UP021 21,25
UP020 21,23
UP019 21,23
UP018 21,25
Family 1047
GM07440
GM07441
GM07555
GM07556
GM07557
GM07558
GM07758
GM07554
GM07439
261 Diplotype Objects
Row Subject 1 2 3 4 5 6 7 8 9 10 11
113 SL-CA128 C/A C G C/C C T/C T/C C/T G C/G C/A
114 SL-CA129 C/A C C/A C/C C T/C T/C C/T G/A C/G G
115 SL-CA130 G C/A A C C T T T T A C G
116 SL-CA132 C/A C C G C/G C T/C T/C C/T C/G C/G C/A
117 SL-CA133 G C C/A C C T T T T C/A C C/A
118 SL-CA137 C/A C G C/G C T/C T/C C/T G C/G G
119 SL-CA138 G C A C C T T T T A C G
120 SL-CA139 G/A C C/A C/G C T/C T/C C/T G/A C/G G
121 SL-CA140 C/A C G/A C/G C T/C T/C C/T G/A C/G G
122 SL-CA141 G C C/A C C T T T T G/A C G
123 SL-CA142 G C A C C T T T T G/A C G
124 SL-CA143 G C A C C T T T T A C G
125 SL-CA144 A C G G C C C C C C G G
126 SL-CA146 A C G G C C C C C C G G
127 SL-CA148 G/A C G/A C/C C T/C T/C C/T G/A C/G G
128 SL-CA151 G C A C C T T T T A C G
129 SL-CA152 C/A C C/A C/G C T/C T/C C/T G/A C/G G
130 SL-CA153 C/A C C/A C/G C T/C T/C C/T G/A C/G G
131 SL-CA154 G C G/A C C T T T T C/A C G
132 SL-CA156 A C C G G C C C C C G G
133 SL-CA160 G C C A C C T T T A C G
134 SL-CA163 G/A C C/A C/G C T/C T/C C/T G/A C/G G
135 SL-CA164 G/A C C/A C/G C T/C T/C C/T C/A C/G G/A
136 SL-CA165 G/A C C/A C/G C T/C T/C C/T C/A C/G G
137 SL-CA166 C/A C C/A C/G C T/C T/C C/T C/A C/G G
12 Haplotype Objects
Row Id 1 2 3 4 5 6 7 8 9 10 11
1 20 A C G C C T T T A C G
2 21 A C G C C T T T A C G
3 22 G A A C C T T T A C G
4 23 G C A C C T T T A C G
5 24 G C A C C T T T G C G
6 25 G C G C C T T T G C A
Project: Asthma
Active Gene: ADRB2
View: Patient Table

FIG. 29B



Row	Patient	Severity	Skin Tes...	FVC LP...	FVC %P...	FEV1 L...	FEV1 %...	FEV1/FV...	FEF PRE	FEF %P...	FVC
1	SL-AA131	2.0	1.0	1.88	58.0	1.28	52.0	68.0	0.83	49.0	1.8
2	SL-AA134	2.0	1.0	2.01	54.0	0.96	34.0	48.0	0.45	12.0	2.2
3	SL-AA136	0.0	0.0	2.56	89.0	2.22	93.0	87.0	3.2	91.0	2.5
4	SL-AA150	2.0	1.0	1.4	50.0	0.6	27.0	43.0	0.22	7.0	1.5
5	SL-AA155	2.0	1.0	1.77	40.0	0.98	27.0	55.0	0.61	16.0	2.2
6	SL-AA159	2.0	1.0	2.89	66.0	1.71	51.0	59.0	0.9	20.0	4.4
7	SL-AA195	1.0	1.0	4.28	96.0	2.7	79.0	63.0	1.48	33.0	5.2
8	SL-AA211	1.0	1.0	3.44	91.0	1.97	66.0	57.0	1.39	32.0	5.5
9	SL-AA227	2.0	0.0	1.93	54.0	0.96	37.0	49.0	0.35	11.0	2.5
10	SL-AA253	1.0	1.0	3.0	96.0	2.01	70.0	57.0	0.99	25.0	3.8
11	SL-AA270	NP	NP	NP	NP	NP	NP	NP	NP	NP	NP
12	SL-AA275	NP	NP	NP	NP	NP	NP	NP	NP	NP	NP
13	SL-CA101	1.0	1.0	2.17	85.0	1.92	64.0	71.0	1.33	38.0	3.2
14	SL-CA103	2.0	1.0	3.56	59.0	2.16	46.0	61.0	1.13	18.0	4.1
15	SL-CA104	2.0	0.0	2.76	57.0	1.46	39.0	53.0	0.59	16.0	3.4
16	SL-CA105	2.0	0.0	1.99	62.0	1.11	46.0	57.0	0.55	24.0	2.3
17	SL-CA106	0.0	1.0	3.46	82.0	2.69	83.0	57.0	2.28	51.0	4.4
18	SL-CA107	0.0	1.0	3.82	113.0	2.59	83.0	78.0	1.7	46.0	3.9
19	SL-CA108	NP	NP	NP	NP	NP	NP	NP	NP	NP	NP
20	SL-CA109	1.0	1.0	2.63	93.0	1.7	7.0	64.5	0.89	25.0	2.8
21	SL-CA110	0.0	1.0	4.56	114.0	3.18	101.0	70.0	2.24	51.0	4.5
22	SL-CA111	2.0	1.0	3.08	69.0	2.01	58.0	65.0	1.12	32.0	3.3
23	SL-CA114	1.0	0.0	2.83	84.0	2.18	77.0	77.0	1.77	43.0	3.0
24	SL-CA116	1.0	1.0	2.44	83.0	1.91	79.0	78.0	1.8	49.0	2.4
25	SL-CA117	1.0	1.0	3.81	90.0	2.25	67.0	59.0	1.04	22.0	4.1
26	SL-CA118	1.0	1.0	1.53	76.0	1.27	71.0	83.0	1.27	49.0	1.6
27	SL-CA119	NP	NP	NP	NP	NP	NP	NP	NP	NP	NP
28	SL-CA120	0.0	1.0	4.24	106.0	2.71	83.0	64.0	1.61	33.0	4.4
29	SL-CA121	1.0	0.0	3.05	88.0	1.9	70.0	62.0	0.95	26.0	3.6
30	SL-CA122	0.0	1.0	5.76	105.0	4.35	103.0	75.5	3.52	62.0	6.0
31	SL-CA123	2.0	1.0	1.82	66.0	0.92	40.0	50.0	0.41	12.0	2.5
32	SL-CA124	2.0	0.0	2.45	59.0	1.3	43.0	53.0	0.41	11.0	2.5
33	SL-CA125	2.0	1.0	1.19	42.0	0.81	37.0	68.0	0.47	22.0	1.3
34	SL-CA126	2.0	0.0	1.74	64.0	1.17	52.0	67.0	0.55	18.0	1.8
35	SL-CA127	1.0	1.0	1.97	68.7	1.63	73.0	83.0	1.49	66.6	2.6

FIG. 30

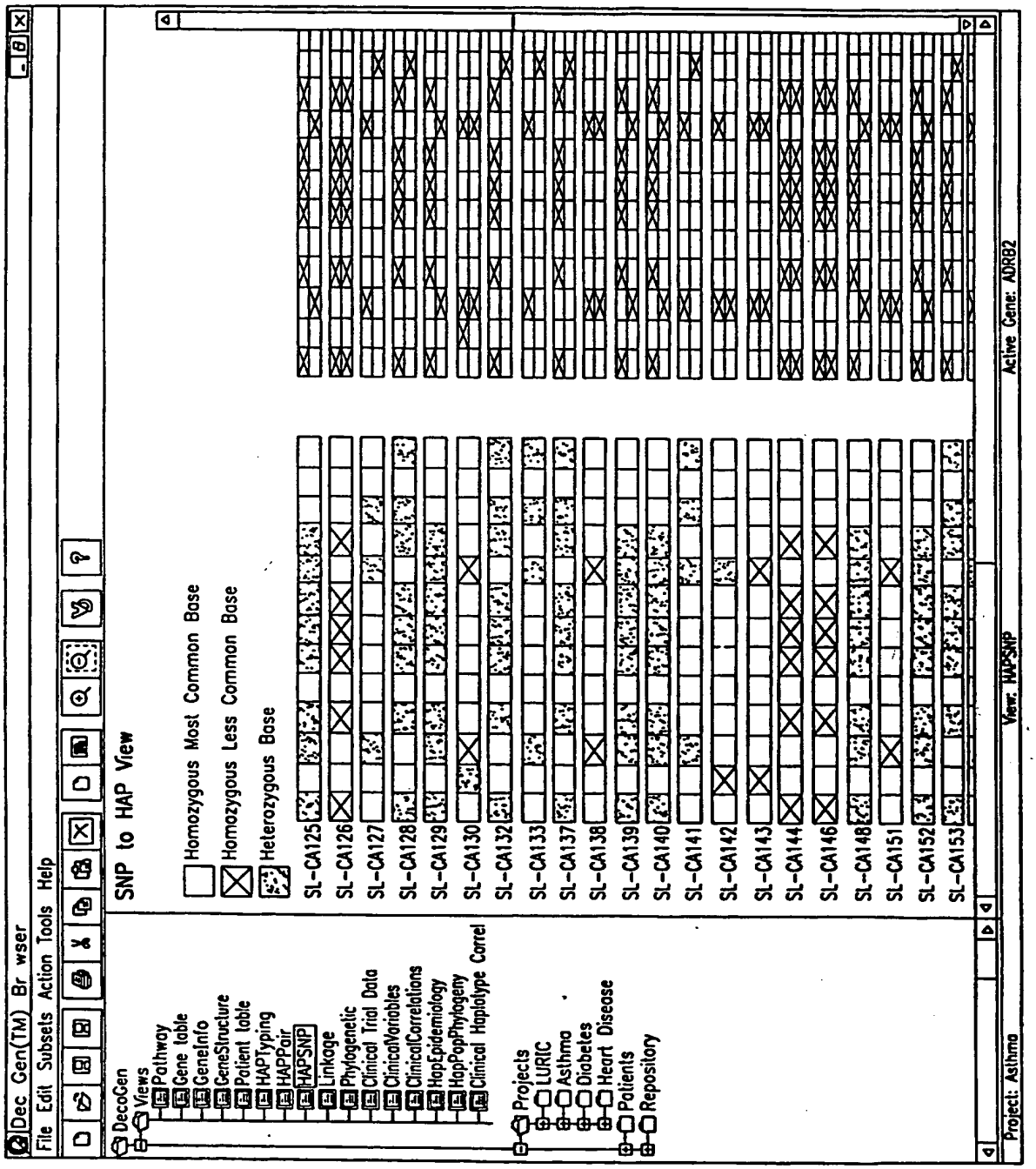

Dec Gen(TM) Br wser
File Edit Subsets Action Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Patients
Repository
SNP to HAP View
Homozygous Most Common Base
Homozygous Less Common Base
Heterozygous Base
SL-CA125
SL-CA126
SL-CA127
SL-CA128
SL-CA129
SL-CA130
SL-CA132
SL-CA133
SL-CA137
SL-CA138
SL-CA139
SL-CA140
SL-CA141
SL-CA142
SL-CA143
SL-CA144
SL-CA146
SL-CA148
SL-CA151
SL-CA152
SL-CA153
Project: Asthma
View: HAPSNP
Active Gene: ADRB2

FIG. 31

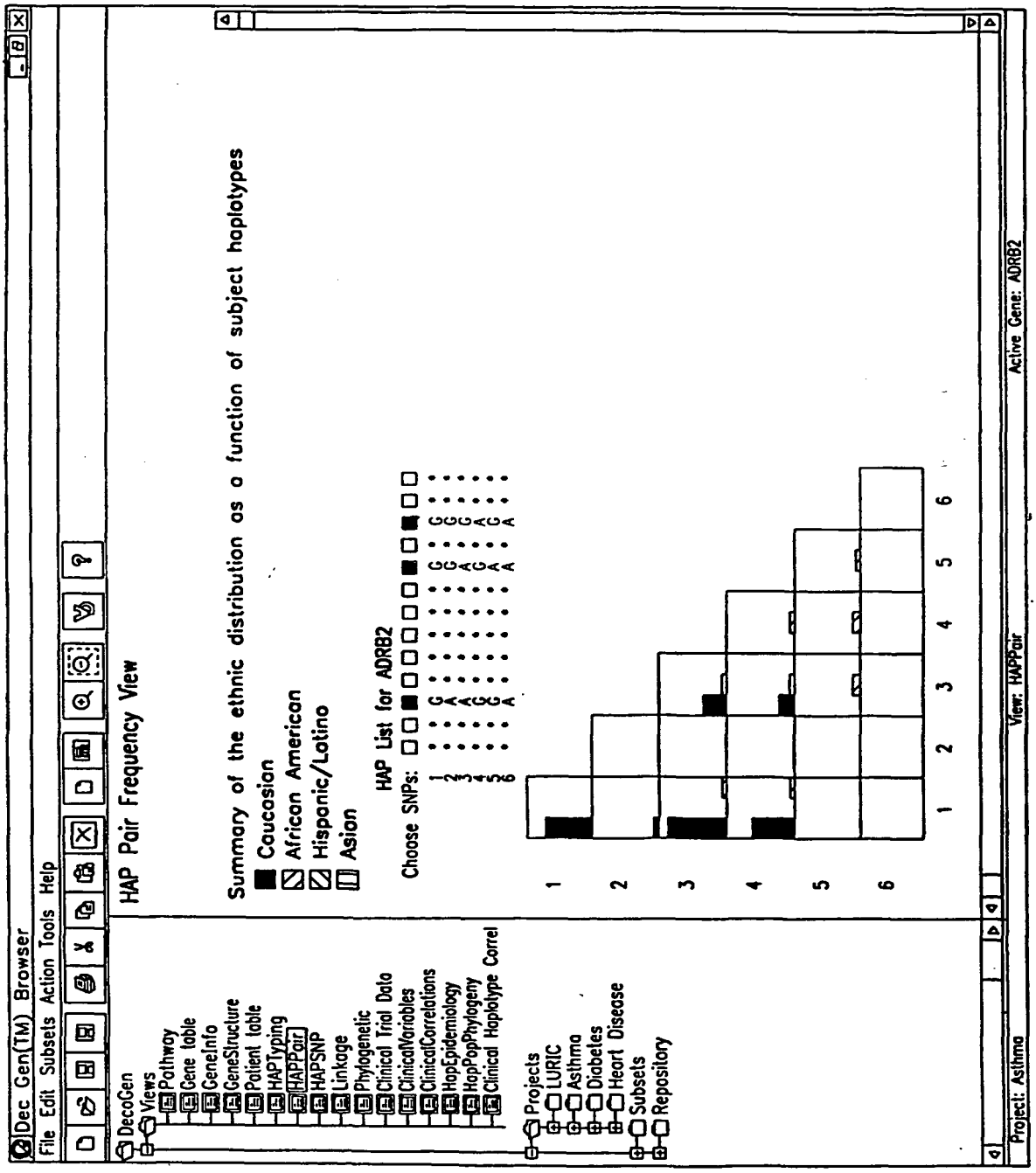

Dec Gen(TM) Browser
File Edit Subsets Action Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Subsets
Repository
HAP Pair Frequency View
Summary of the ethnic distribution as a function of subject haplotypes
Caucasion
African American
Hispanic/Latino
Asian
HAP List for ADRB2
Choose SNPs:
1 G G
2 A G
3 C C
4 G G
5 C C
6 A A
1 2 3 4 5 6
View: HAPPair
Active Gene: ADRB2
Project: Asthma

FIG. 32

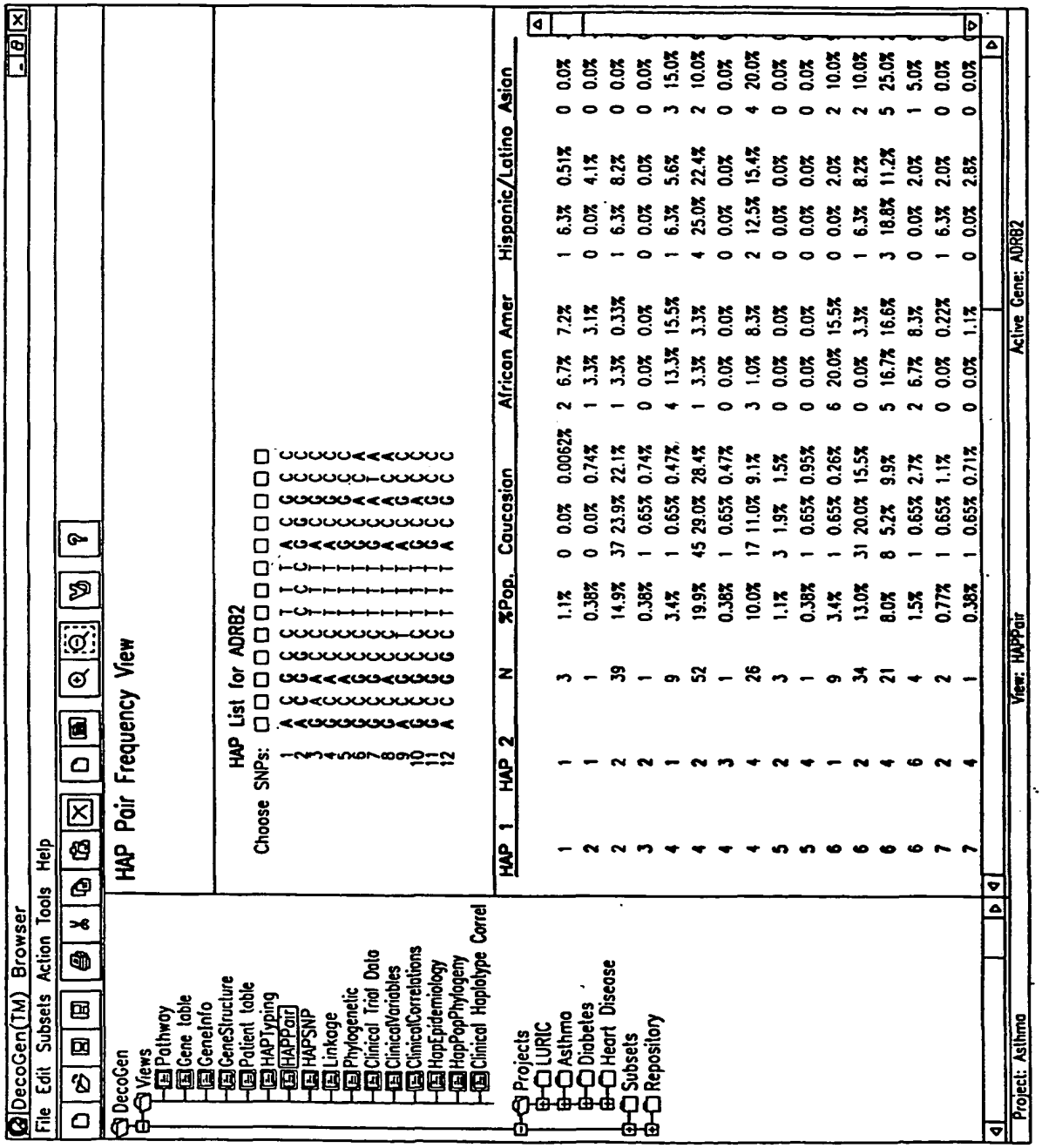
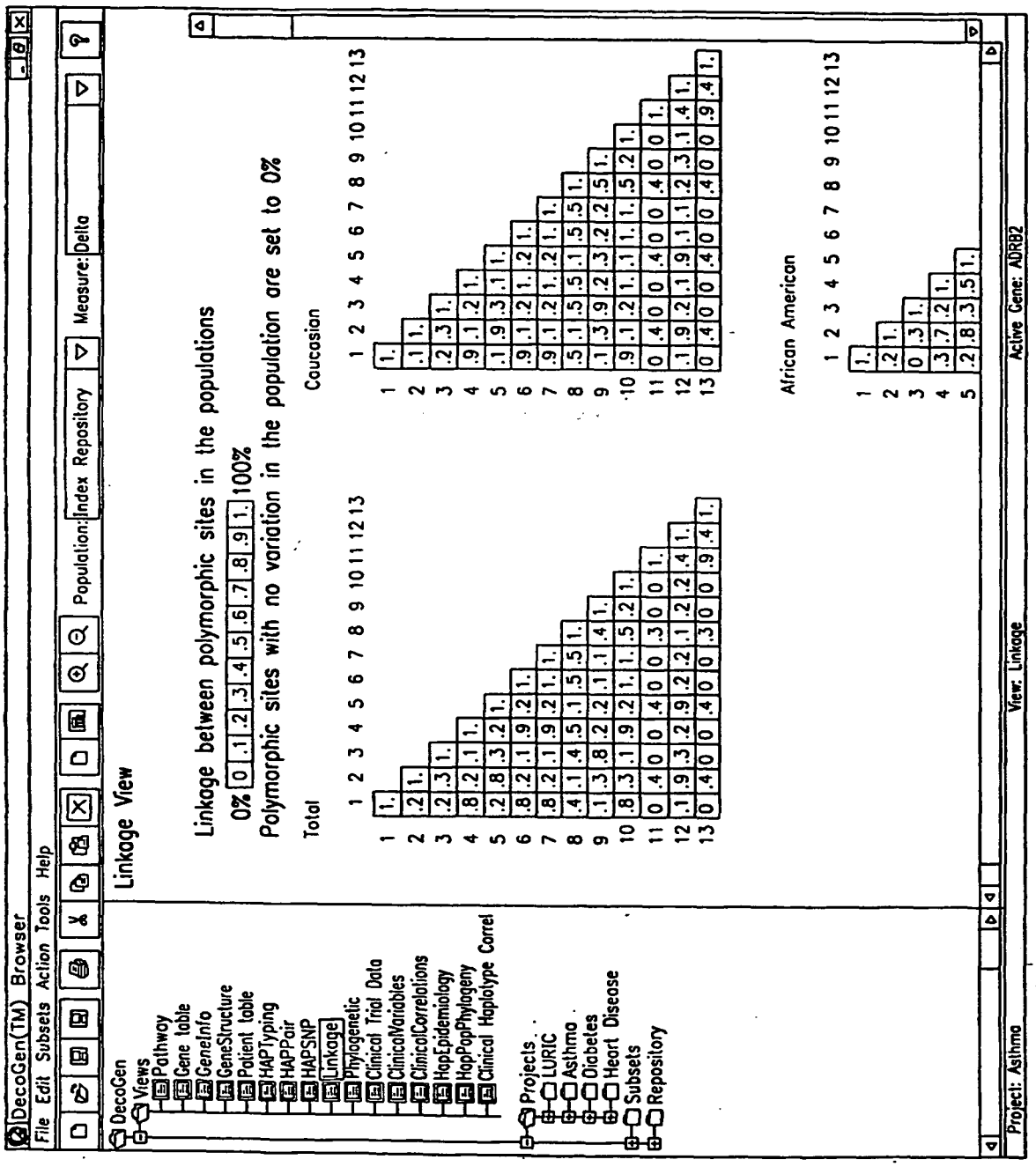

DecoGen(TM) Browser
File Edit Subsets Action Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Subsets
Repository
HAP Pair Frequency View
HAP List for ADRB2
Choose SNPs:
HAP 1 HAP 2 N %Pop. Caucasion African Amer Hispanic/Latino Asian
Project: Asthma
View: HAPPair
Active Gene: ADRB2

FIG. 33


DecoGen(TM) Browser
File Edit Subsets Action Tools Help
Population: Index Repository
Measure: Delta
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Subsets
Repository
Linkage View
Linkage between polymorphic sites in the populations
0% 0 .1 .2 .3 .4 .5 .6 .7 .8 .9 1. 100%
Polymorphic sites with no variation in the population are set to 0%
Total
Caucasian
African American
1 2 3 4 5 6 7 8 9 10 11 12 13
Project: Asthma
View: Linkage
Active Gene: ADRB2

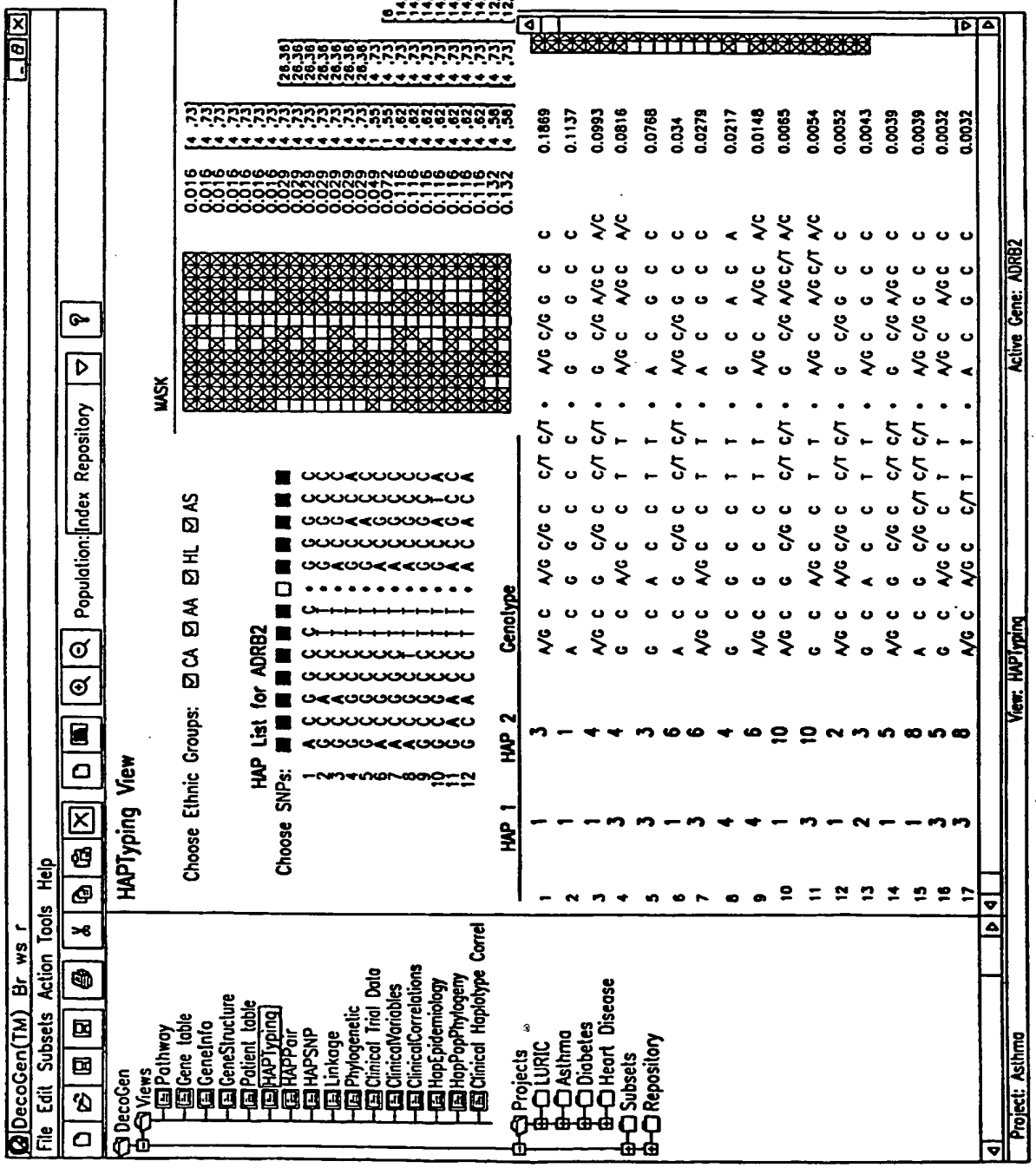

DecoGen(TM) Br ws r
File Edit Subsets Action Tools Help
Population: Index Repository
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Subsets
Repository
HAPTyping View
Choose Ethnic Groups: CA AA HL AS
HAP List for ADRB2
Choose SNPs:
MASK
HAP 1 HAP 2 Genotype
Project: Asthma
View: HAPTyping
Active Gene: ADRB2

FIG. 34

FIG. 35

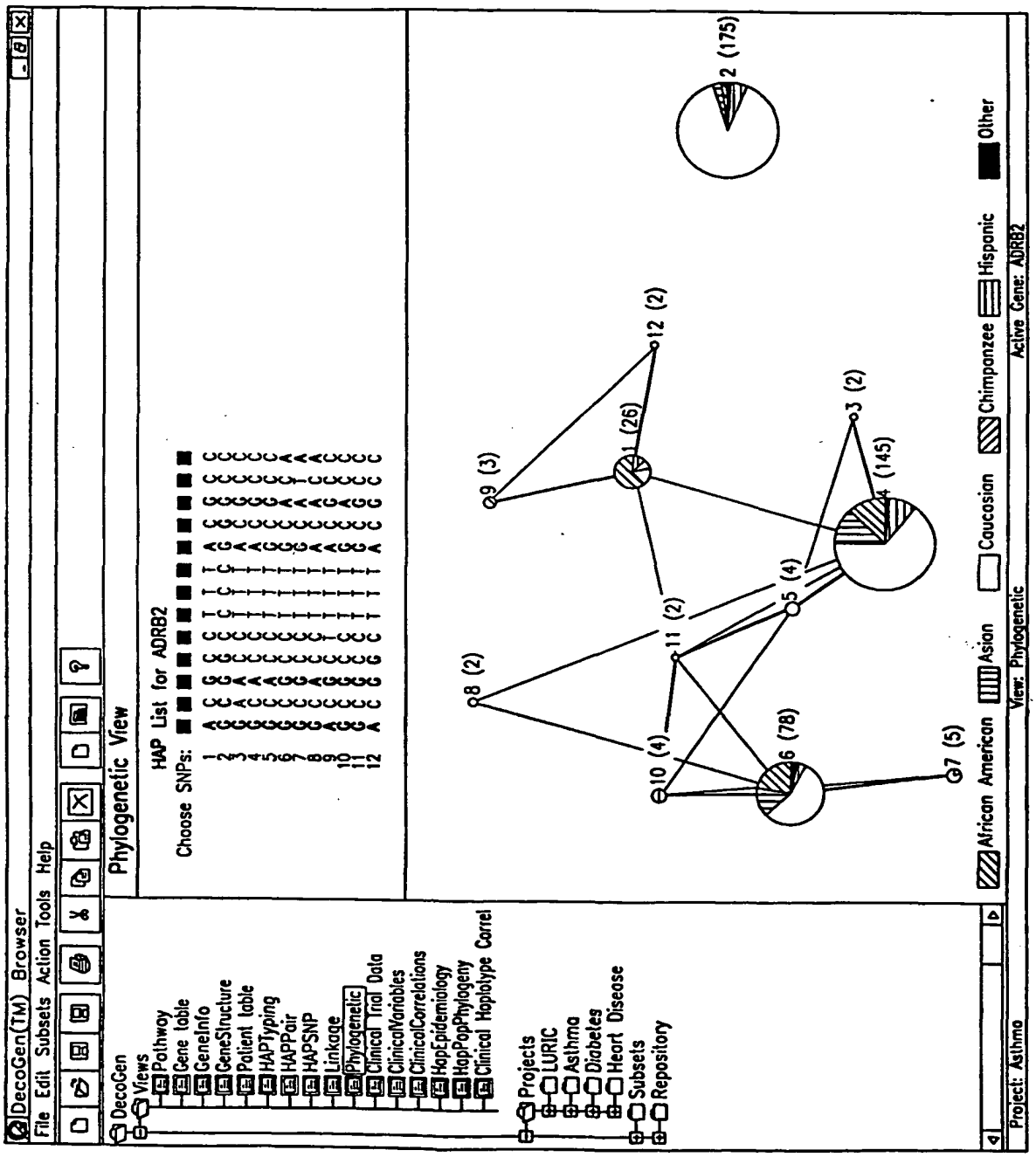

DecoGen(TM) Browser
File Edit Subsets Action Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Subsets
Repository
Phylogenetic View
HAP List for ADRB2
Choose SNPs:
1 2 3 4 5 6 8 9 10 11 12
2 (175)
12 (2)
1 (26)
9 (3)
3 (2)
4 (145)
5 (4)
11 (2)
8 (2)
10 (4)
6 (78)
7 (5)
African American
Asian
Caucasian
Chimpanzee
Hispanic
Other
View: Phylogenetic
Active Gene: ADRB2
Project: Asthma

FIG. 36

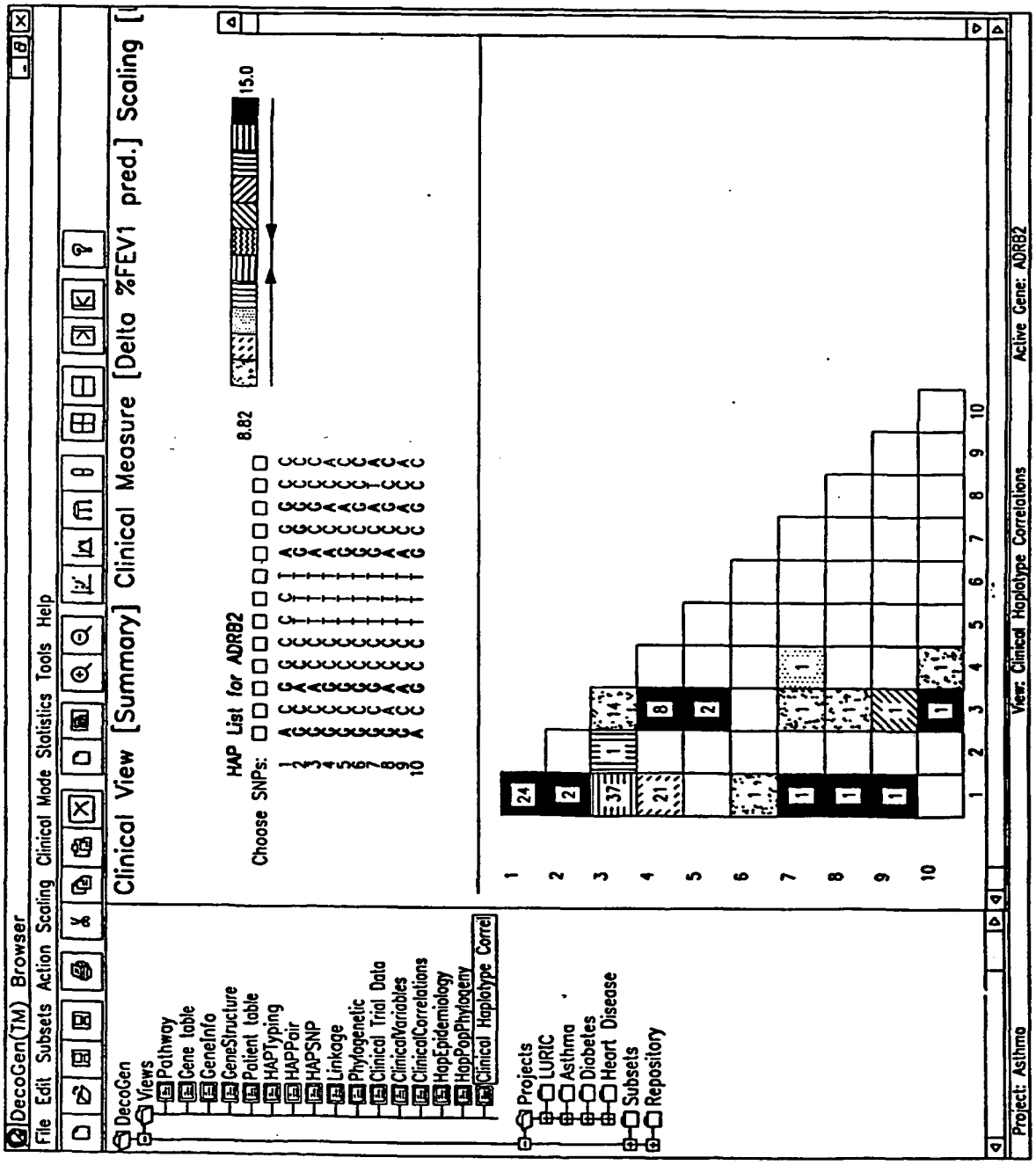
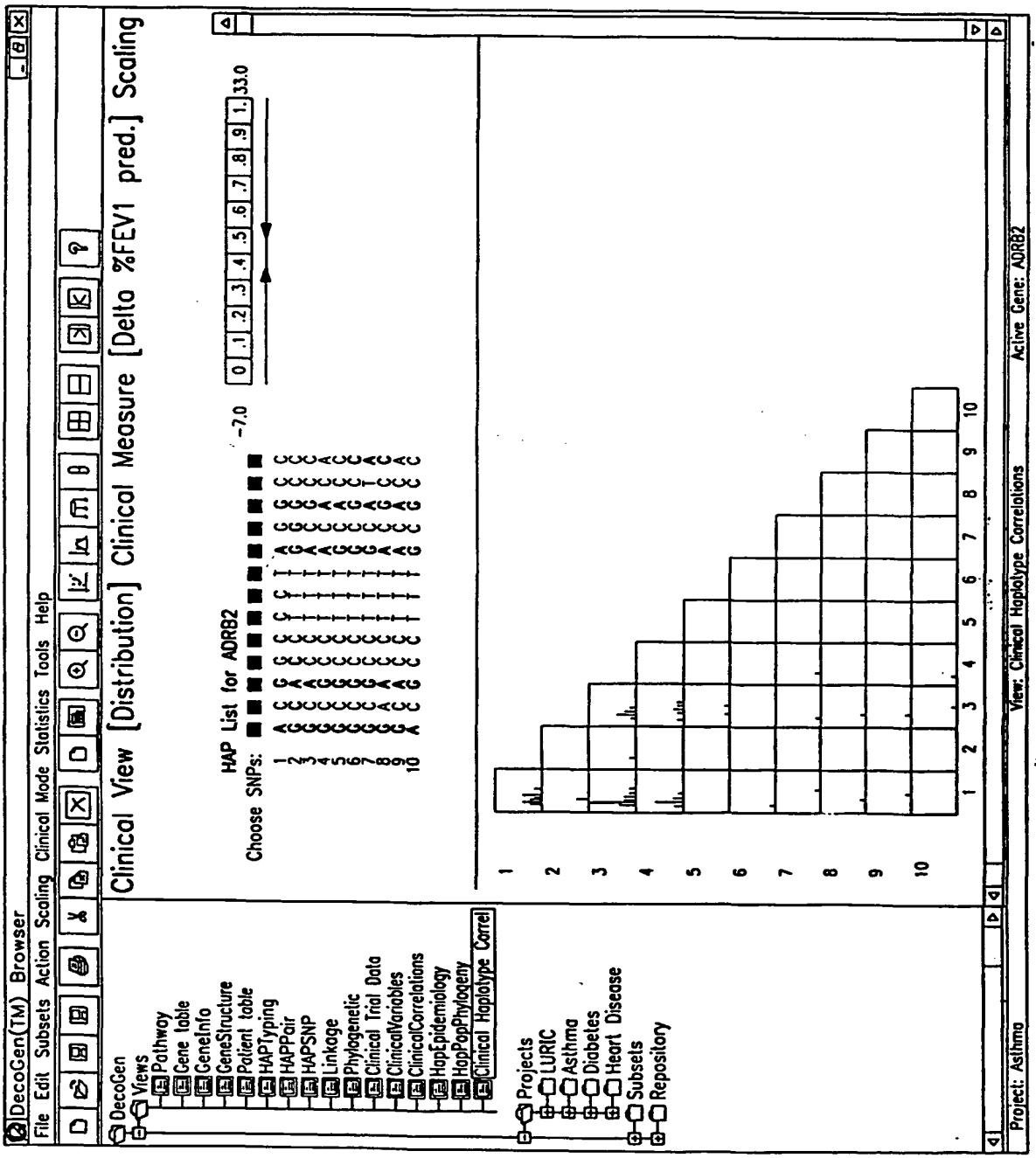

DecoGen(TM) Browser
File Edit Subsets Action Scaling Clinical Mode Statistics Tools Help
Clinical View [Summary] Clinical Measure [Delta %FEV1 pred.] Scaling [
HAP List for ADRB2
Choose SNPs:
8.82
15.0
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Subsets
Repository
View: Clinical Haplotype Correlations
Active Gene: ADRB2
Project: Asthma

FIG. 37


DecoGen(TM) Browser
File Edit Subsets Action Scaling Clinical Mode Statistics Tools Help
Clinical View [Distribution] Clinical Measure [Delta %FEV1 pred.] Scaling
HAP List for ADRB2
Choose SNPs:
-7.0
33.0
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical HapIotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Subsets
Repository
Project: Asthma
View: Clinical HapIotype Correlations
Active Gene: ADRB2

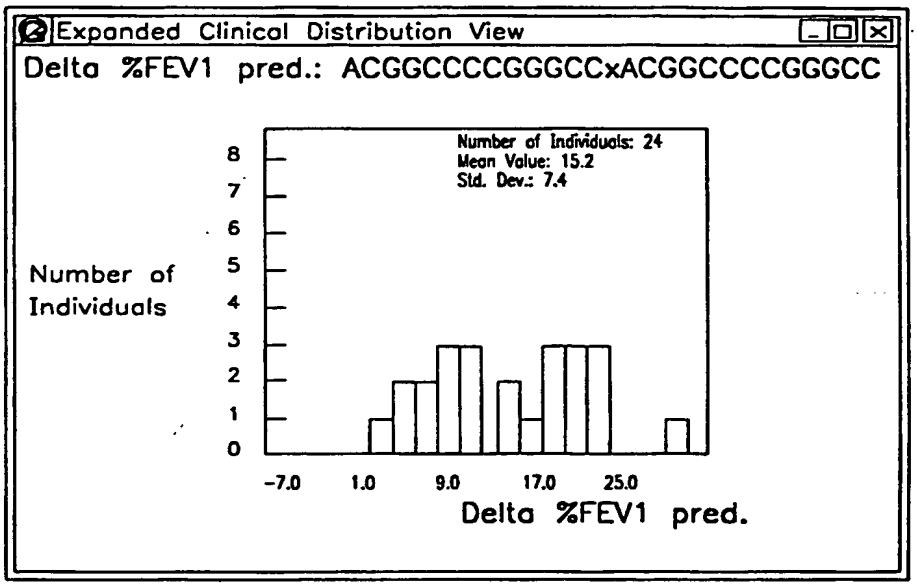

Expanded Clinical Distribution View
Delta %FEV1 pred.: ACGGCCCCGGGCCxACGGCCCCGGGCC
Number of Individuals: 24
Mean Value: 15.2
Std. Dev.: 7.4
Number of Individuals
8
7
6
5
4
3
2
1
0
-7.0
1.0
9.0
17.0
25.0
Delta %FEV1 pred.

FIG. 38

DecoGen Single Gene Statistics Calculator

File

Show/Hide | CC Line

Gene: adrenergic, beta-2-, receptor, surface Clinical Measure: Delta %FEV1 pr d.

Confidence: 0.05 0.1 Fixed Site: -4

Regression Results

Marker	Intercept	Slope	Slope Range		R**2	Corr. Coef (R)	P-value
G********	10.501	1.99	-0.08	4.06	0.0301	0.1734	0.0297
********G****	10.526	1.956	-0.11	4.02	0.0293	0.1711	0.0314
********A*G**	14.583	-2.206	-4.28	-0.13	0.0365	-0.1911	0.0187
A***A****	14.471	-2.048	-4.13	0.032	0.0315	-0.1774	0.0268
A*****G**	14.626	-2.241	-4.32	-0.16	0.0374	-0.1934	0.0175
A***A*G**	14.615	-2.308	-4.4	-0.21	0.0391	-0.1977	0.0156
GCACCTTTACGCC	14.6	-2.343	-4.46	-0.22	0.0394	-0.1984	0.0153

FIG. 39A

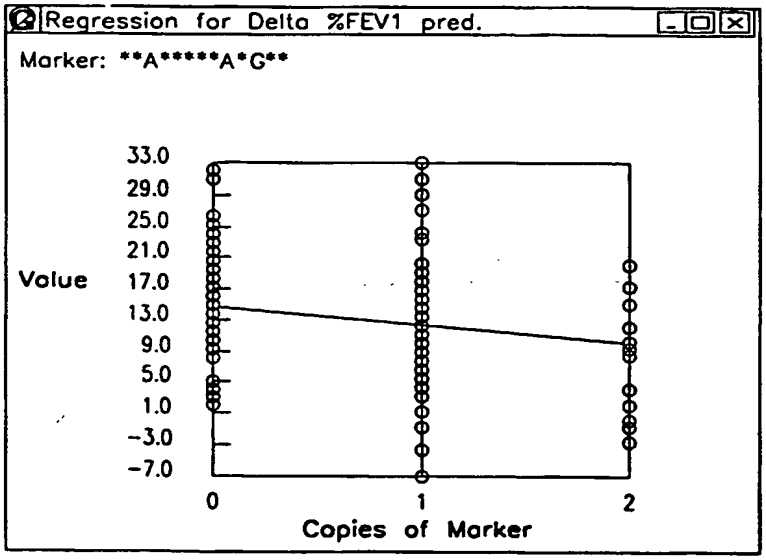
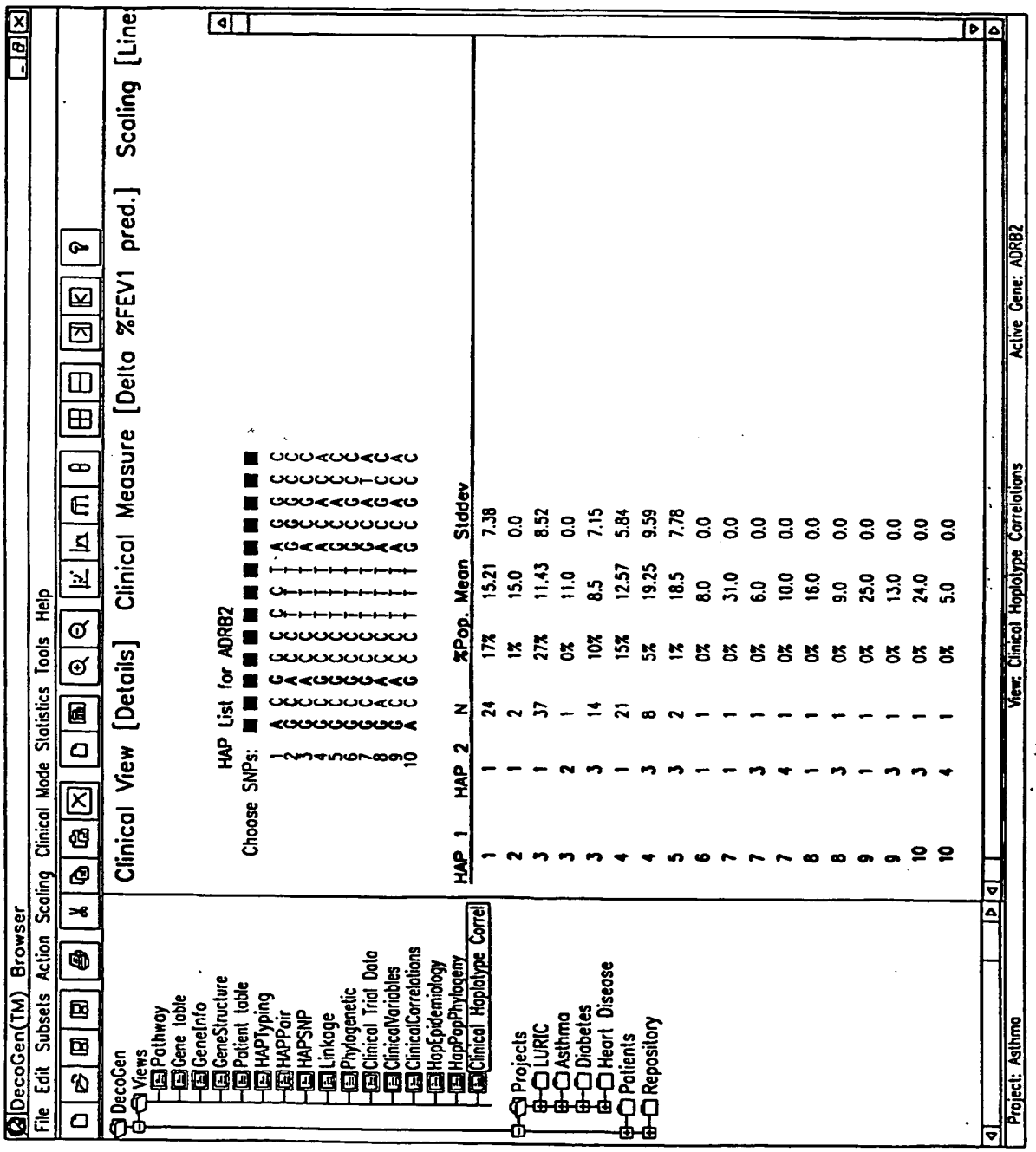

Regression for Delta %FEV1 pred.
Marker: **A*****A*G**
Value
33.0
29.0
25.0
21.0
17.0
13.0
9.0
5.0
1.0
-3.0
-7.0
0
1
2
Copies of Marker

FIG. 39B

FIG. 40


DecoGen(TM) Browser
File Edit Subsets Action Scaling Clinical Mode Statistics Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Patients
Repository
Clinical View [Details] Clinical Measure [Delta %FEV1 pred.] Scaling [Line
HAP List for ADRB2
Choose SNPs:
HAP 1 HAP 2 N %Pop. Mean Stddev
1 1 24 17% 15.21 7.38
2 1 2 1% 15.0 0.0
3 1 37 27% 11.43 8.52
3 2 1 0% 11.0 0.0
3 3 14 10% 8.5 7.15
4 1 21 15% 12.57 5.84
4 3 8 5% 19.25 9.59
5 3 2 1% 18.5 7.78
6 1 1 0% 8.0 0.0
7 1 1 0% 31.0 0.0
7 3 1 0% 6.0 0.0
7 4 1 0% 10.0 0.0
8 1 1 0% 16.0 0.0
8 3 1 0% 9.0 0.0
9 1 1 0% 25.0 0.0
9 3 1 0% 13.0 0.0
10 3 1 0% 24.0 0.0
10 4 1 0% 5.0 0.0
Project: Asthma
View: Clinical Haplotype Correlations
Active Gene: ADRB2

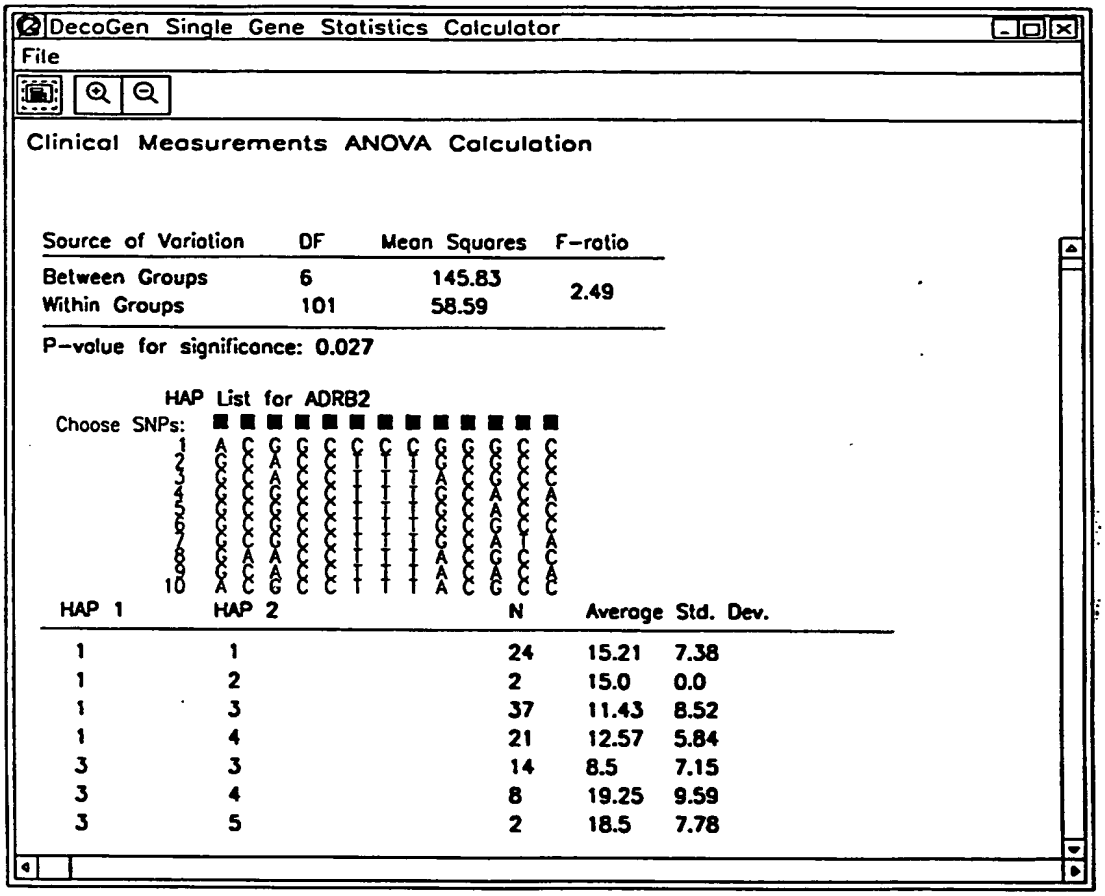

DecoGen Single Gene Statistics Calculator
File
Clinical Measurements ANOVA Calculation
Source of Variation DF Mean Squares F-ratio
Between Groups 6 145.83 2.49
Within Groups 101 58.59
P-value for significance: 0.027
HAP List for ADRB2
Choose SNPs:
HAP 1 HAP 2 N Average Std. Dev.
1 1 24 15.21 7.38
1 2 2 15.0 0.0
1 3 37 11.43 8.52
1 4 21 12.57 5.84
3 3 14 8.5 7.15
3 4 8 19.25 9.59
3 5 2 18.5 7.78

FIG. 41

FIG. 42

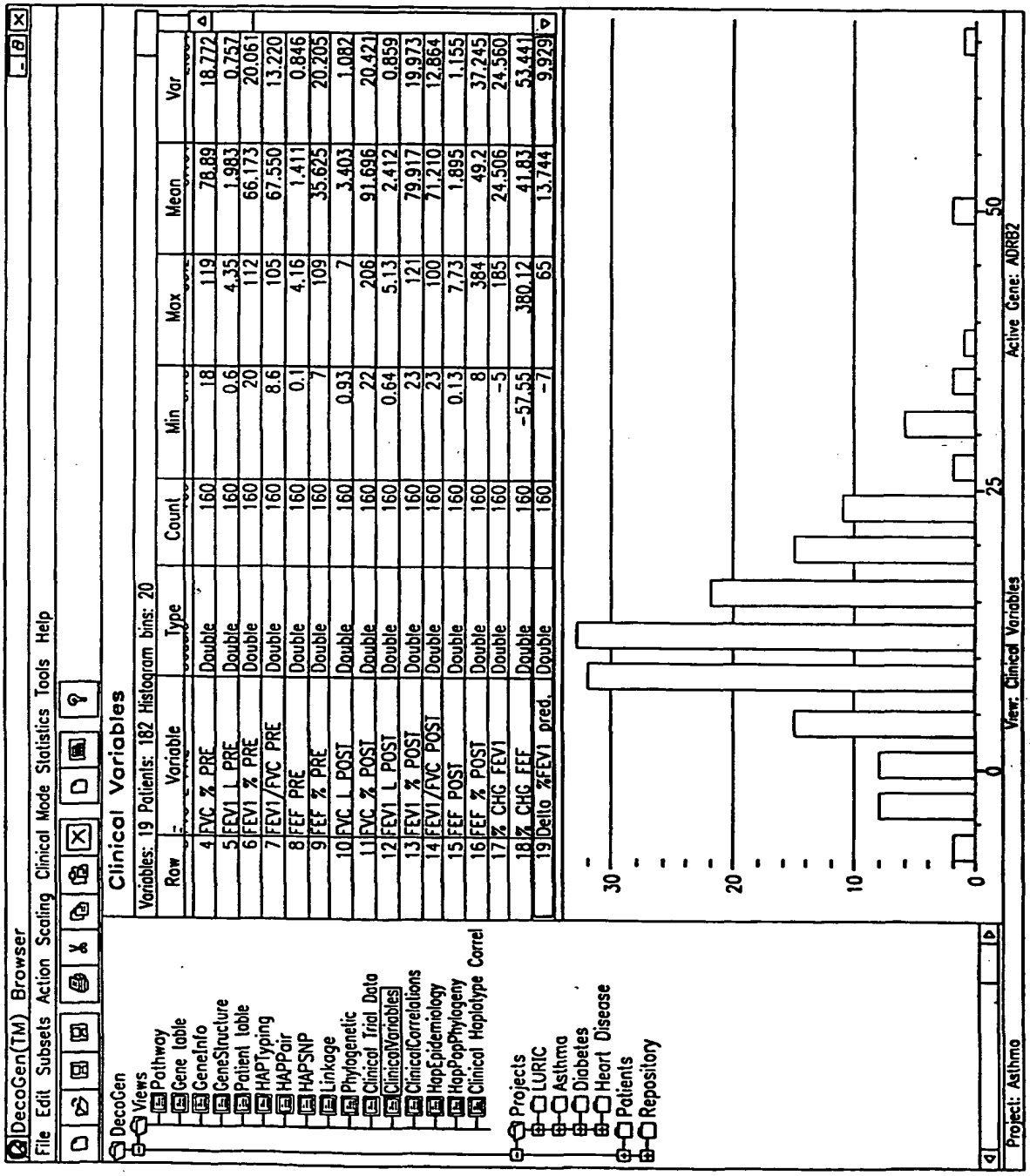
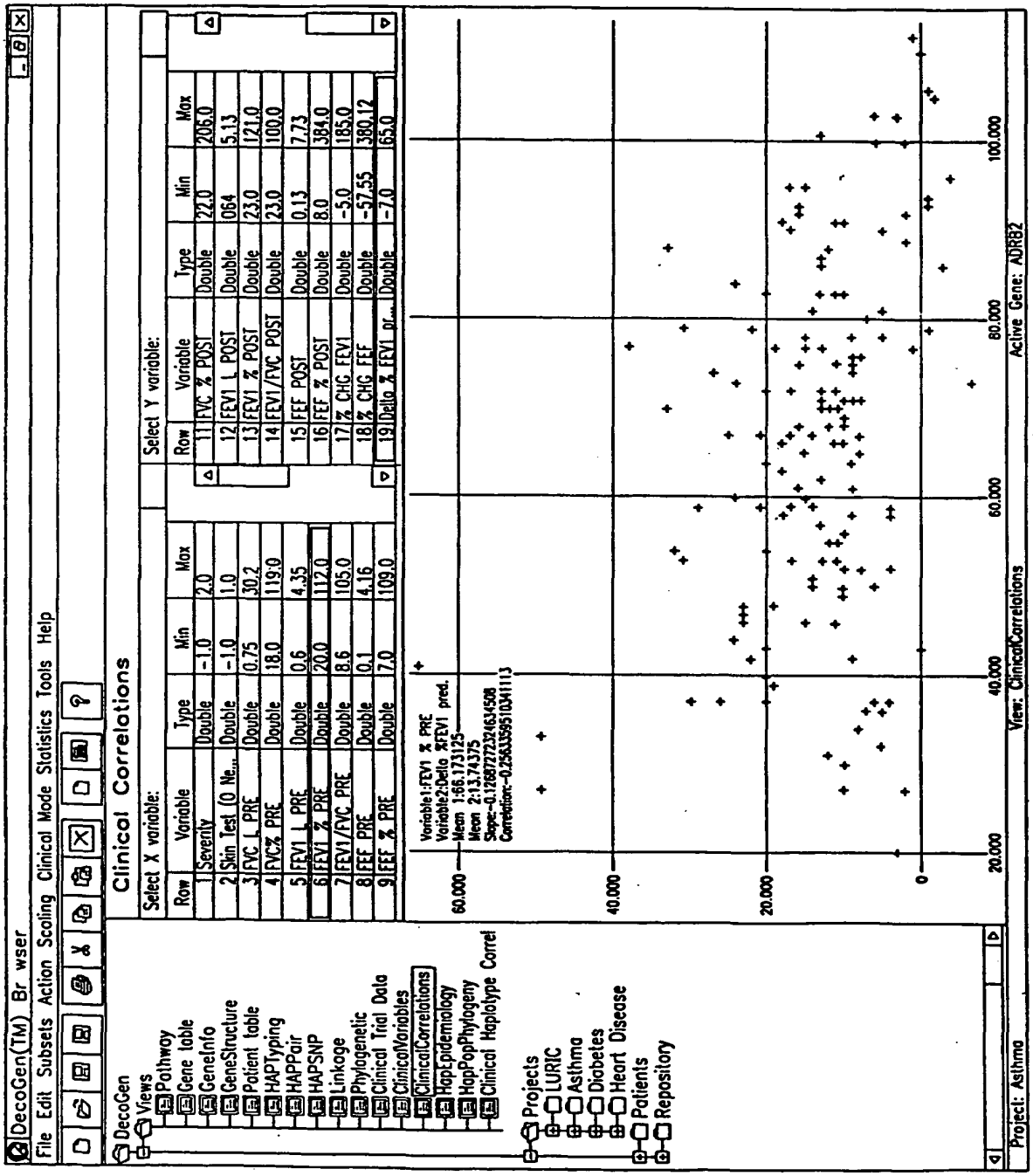

DecoGen(TM) Browser
File Edit Subsets Action Scaling Clinical Mode Statistics Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Patients
Repository
Clinical Variables
Variables: 19 Patients: 182 Histogram bins: 20
Row
Variable
Type
Count
Min
Max
Mean
Var
4 FVC % PRE Double 160 18 119 78.89 18.772
5 FEV1 L PRE Double 160 0.6 4.35 1.983 0.757
6 FEV1 % PRE Double 160 20 112 66.173 20.061
7 FEV1/FVC PRE Double 160 8.6 105 67.550 13.220
8 FEF PRE Double 160 0.1 4.16 1.411 0.846
9 FEF % PRE Double 160 7 109 35.625 20.205
10 FVC L POST Double 160 0.93 7 3.403 1.082
11 FVC % POST Double 160 22 206 91.696 20.421
12 FEV1 L POST Double 160 0.64 5.13 2.412 0.859
13 FEV1 % POST Double 160 23 121 79.917 19.973
14 FEV1/FVC POST Double 160 23 100 71.210 12.864
15 FEF POST Double 160 0.13 7.73 1.895 1.155
16 FEF % POST Double 160 8 384 49.2 37.245
17 % CHG FEV1 Double 160 -5 185 24.506 24.560
18 % CHG FEF Double 160 -57.55 380.12 41.83 53.441
19 Delta %FEV1 pred. Double 160 -7 65 13.744 9.929
30
20
10
0
0
25
50
Project: Asthma
View: Clinical Variables
Active Gene: ADRB2

FIG. 43


DecoGen(TM) Br wser
File Edit Subsets Action Scaling Clinical Mode Statistics Tools Help
DecoGen
Views
Pathway
Gene Table
GeneInfo
GeneStructure
Patient Table
HAPTyping
HAPPair
HAPSNP
Linkage
Phylogenetic
Clinical Trial Data
ClinicalVariables
ClinicalCorrelations
HapEpidemiology
HapPopPhylogeny
Clinical Haplotype Correl
Projects
LURIC
Asthma
Diabetes
Heart Disease
Patients
Repository
Clinical Correlations
Select X variable:
Row Variable Type Min Max
1 Severity Double -1.0 2.0
2 Skin Test (0 Ne... Double -1.0 1.0
3 FVC_L_PRE Double 0.75 30.2
4 FVC% PRE Double 18.0 119.0
5 FEV1_L_PRE Double 0.6 4.35
6 FEV1_%_PRE Double 20.0 112.0
7 FEV1/FVC_PRE Double 8.6 105.0
8 FEF_PRE Double 0.1 4.16
9 FEF_%_PRE Double 7.0 109.0
Select Y variable:
Row Variable Type Min Max
11 FVC_%_POST Double 22.0 206.0
12 FEV1_L_POST Double 064 5.13
13 FEV1_%_POST Double 23.0 121.0
14 FEV1/FVC POST Double 23.0 100.0
15 FEF_POST Double 0.13 7.73
16 FEF_%_POST Double 8.0 384.0
17 %_CHG_FEV1 Double -5.0 185.0
18 %_CHG_FEF Double -57.55 380.12
19 Delta_%_FEV1_pr... Double -7.0 65.0
Variable1:FEV1_%_PRE
Variable2:Delta %FEV1 pred.
Mean 1:66.173125
Mean 2:13.74375
Slope:-0.12687723246345O8
Correlation:-0.25633595103411113
60.000
40.000
20.000
0
20.000
40.000
60.000
80.000
100.000
View: ClinicalCorrelations
Active Gene: ADRB2
Project: Asthma

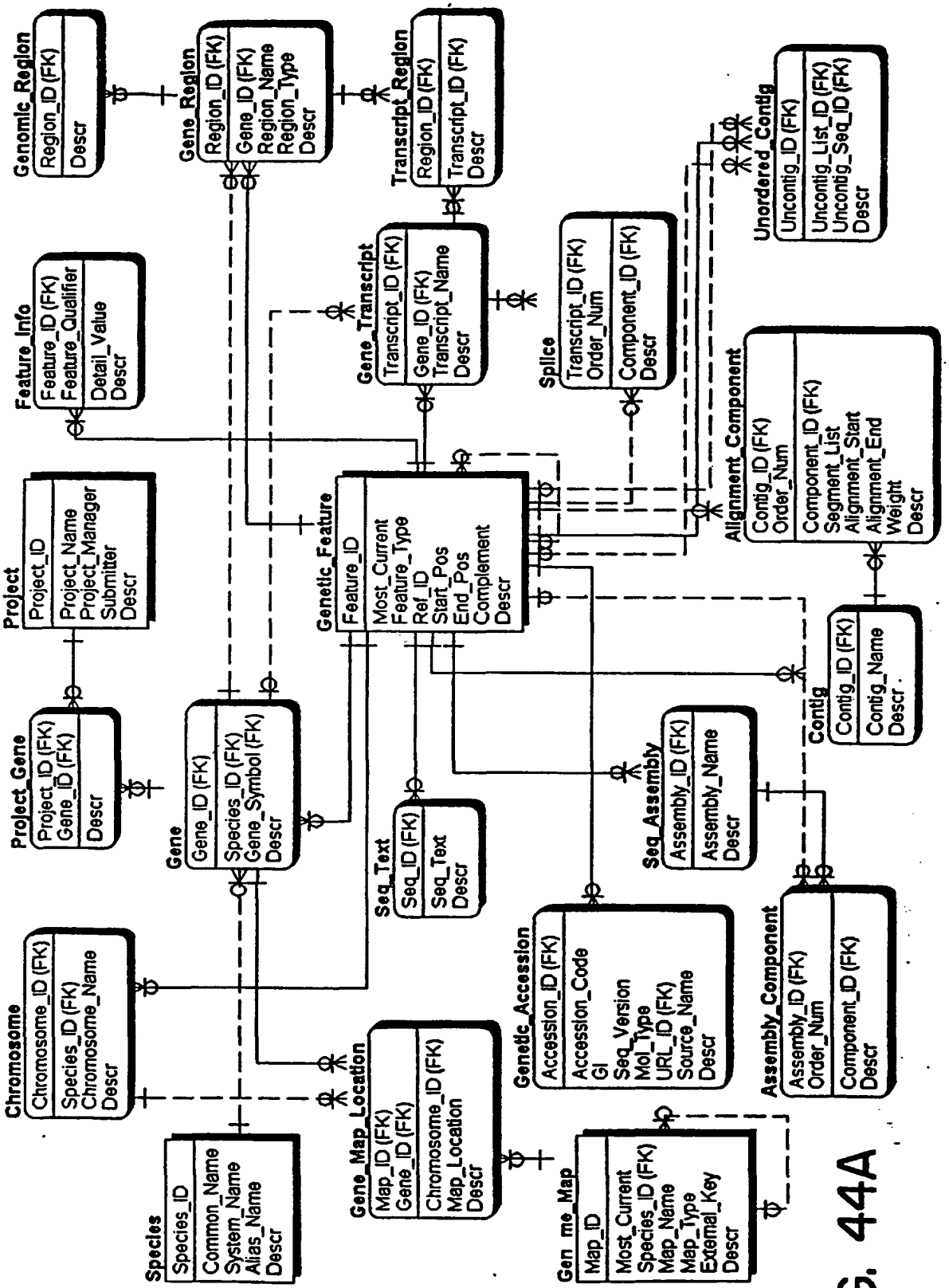

Genomic_Region
Region_ID (FK)
Descr
Gene_Region
Region_ID (FK)
Gene_ID (FK)
Region_Name
Region_Type
Descr
Transcript_Region
Region_ID (FK)
Transcript_ID (FK)
Descr
Unordered_Contig
Uncontig_ID (FK)
Uncontig_List_ID (FK)
Uncontig_Seq_ID (FK)
Descr
Feature_Info
Feature_ID (FK)
Feature_Qualifier
Detail_Value
Descr
Gene_Transcript
Transcript_ID (FK)
Gene_ID (FK)
Transcript_Name
Descr
Splice
Transcript_ID (FK)
Order_Num
Component_ID (FK)
Descr
Alignment_Component
Contig_ID (FK)
Order_Num
Component_ID (FK)
Segment_List
Aligment_Start
Aligment_End
Weight
Descr
Project
Project_ID
Project_Name
Project_Manager
Submitter
Descr
Genetic_Feature
Feature_ID
Most_Current
Feature_Type
Ref_ID
Start_Pos
End_Pos
Complement
Descr
Contig
Contig_ID (FK)
Contig_Name
Descr
Project_Gene
Project_ID (FK)
Gene_ID (FK)
Descr
Gene
Gene_ID (FK)
Species_ID (FK)
Gene_Symbol (FK)
Descr
Seq_Text
Seq_ID (FK)
Seq_Text
Descr
Seq_Assembly
Assembly_ID (FK)
Assembly_Name
Descr
Chromosome
Chromosome_ID (FK)
Species_ID (FK)
Chromosome_Name
Descr
Gene_Map_Location
Map_ID (FK)
Gene_ID (FK)
Chromosome_ID (FK)
Map_Location
Descr
Genetic_Accession
Accession_ID (FK)
Accession_Code
GI
Seq_Version
Mol_Type
URL_ID (FK)
Source_Name
Descr
Assembly_Component
Assembly_ID (FK)
Order_Num
Component_ID (FK)
Descr
Species
Species_ID
Common_Name
System_Name
Alias_Name
Descr
Gen me_Map
Map_ID
Most_Current
Species_ID (FK)
Map_Name
Map_Type
External_Key
Descr

FIG. 44A

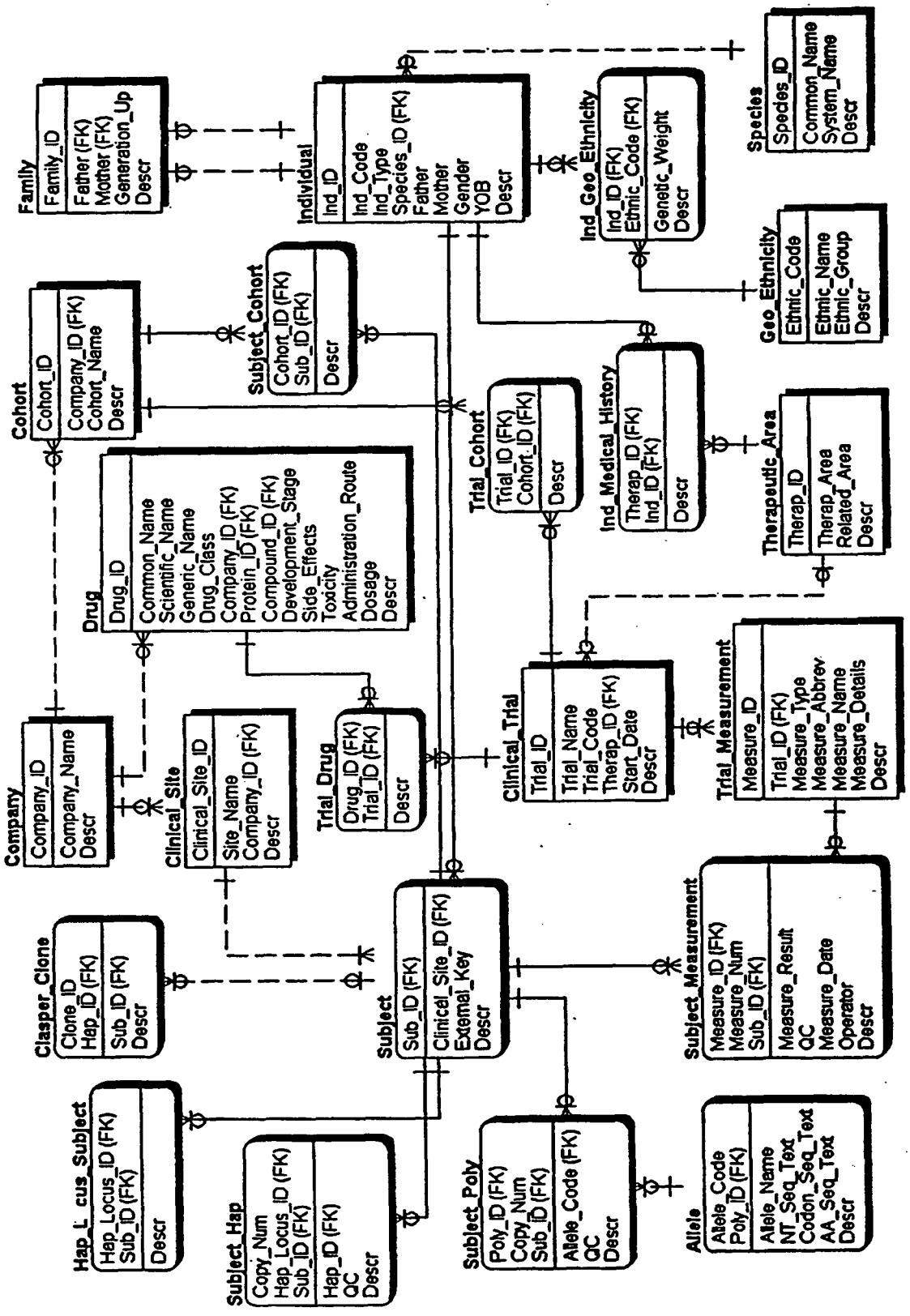

Family
Family_ID
Father (FK)
Mother (FK)
Generation_Up
Descr
Individual
Ind_ID
Ind_Code
Ind_Type
Species_ID (FK)
Father
Mother
Gender
YOB
Descr
Ind_Geo_Ethnicity
Ind_ID (FK)
Ethnic_Code (FK)
Genetic_Weight
Descr
Species
Species_ID
Common_Name
System_Name
Descr
Geo_Ethnicity
Ethnic_Code
Ethnic_Name
Ethnic_Group
Descr
Subject_Cohort
Cohort_ID (FK)
Sub_ID (FK)
Descr
Cohort
Cohort_ID
Company_ID (FK)
Cohort_Name
Descr
Trial_Cohort
Trial_ID (FK)
Cohort_ID (FK)
Descr
Ind_Medical_History
Therap_ID (FK)
Ind_ID (FK)
Descr
Therapeutic_Area
Therap_ID
Therap_Area
Related_Area
Descr
Drug
Drug_ID
Common_Name
Scientific_Name
Generic_Name
Drug_Class
Company_ID (FK)
Protein_ID (FK)
Compound_ID (FK)
Development_Stage
Side_Effects
Toxicity
Administration_Route
Dosage
Descr
Company
Company_ID
Company_Name
Descr
Clinical_Site
Clinical_Site_ID
Site_Name
Company_ID (FK)
Descr
Trial_Drug
Drug_ID (FK)
Trial_ID (FK)
Descr
Clinical_Trial
Trial_ID
Trial_Name
Trial_Code
Therap_ID (FK)
Start_Date
Descr
Trial_Measurement
Measure_ID
Trial_ID (FK)
Measure_Type
Measure_Abbrev
Measure_Name
Measure_Details
Descr
Clasper_Clone
Clone_ID
Hap_ID (FK)
Sub_ID (FK)
Descr
Subject
Sub_ID (FK)
Clinical_Site_ID (FK)
External_Key
Descr
Subject_Measurement
Measure_ID (FK)
Measure_Num
Sub_ID (FK)
Measure_Result
QC
Measure_Date
Operator
Descr
Hap_Locus_Subject
Hap_Locus_ID (FK)
Sub_ID (FK)
Descr
Subject_Hap
Copy_Num
Hap_Locus_ID (FK)
Sub_ID (FK)
Hap_ID (FK)
QC
Descr
Subject_Poly
Poly_ID (FK)
Copy_Num
Sub_ID (FK)
Allele_Code (FK)
QC
Descr
Allele
Allele_Code
Poly_ID (FK)
Allele_Name
NT_Seq_Text
Codon_Seq_Text
AA_Seq_Text
Descr

FIG. 44B

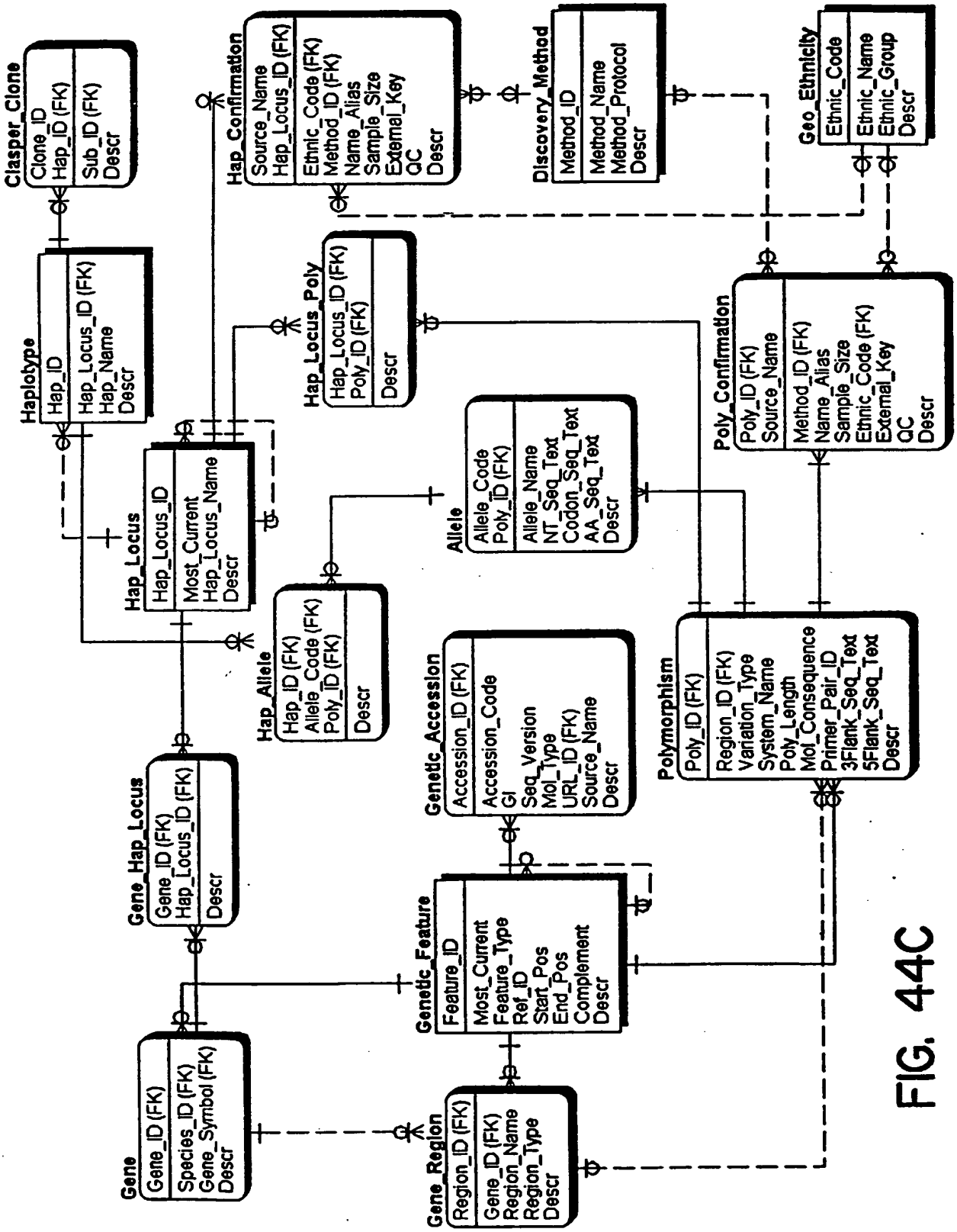

Clasper_Clone
Clone_ID
Hap_ID (FK)
Sub_ID (FK)
Descr
Hap_Confirmation
Source_Name
Hap_Locus_ID (FK)
Ethnic_Code (FK)
Method_ID (FK)
Name_Alias
Sample_Size
Extemal_Key
QC
Descr
Discovery_Method
Method_ID
Method_Name
Method_Protocol
Descr
Geo_Ethnicity
Ethnic_Code
Ethnic_Name
Ethnic_Group
Descr
Haplotype
Hap_ID
Hap_Locus_ID (FK)
Hap_Name
Descr
Hap_Locus_Poly
Hap_Locus_ID (FK)
Poly_ID (FK)
Descr
Poly_Confirmation
Poly_ID (FK)
Source_Name
Method_ID (FK)
Name_Alias
Sample_Size
Ethnic_Code (FK)
Extemal_Key
QC
Descr
Hap_Locus
Hap_Locus_ID
Most_Current
Hap_Locus_Name
Descr
Allele
Allele_Code
Poly_ID (FK)
Allele_Name
NT_Seq_Text
Codon_Seq_Text
AA_Seq_Text
Descr
Hap_Allele
Hap_ID (FK)
Allele_Code (FK)
Poly_ID (FK)
Descr
Genetic_Accession
Accession_ID (FK)
Accession_Code
GI
Seq_Version
Mol_Type
URL_ID (FK)
Source_Name
Descr
Polymorphism
Poly_ID (FK)
Region_ID (FK)
Variation_Type
System_Name
Poly_Length
Mol_Consequence
Primer_Pair_ID
3Flank_Seq_Text
5Flank_Seq_Text
Descr
Gene_Hap_Locus
Gene_ID (FK)
Hap_Locus_ID (FK)
Descr
Genetic_Feature
Feature_ID
Most_Current
Feature_Type
Ref_ID
Start_Pos
End_Pos
Complement
Descr
Gene
Gene_ID (FK)
Species_ID (FK)
Gene_Symbol (FK)
Descr
Gene_Region
Region_ID (FK)
Gene_ID (FK)
Region_Name
Region_Type
Descr

FIG. 44C

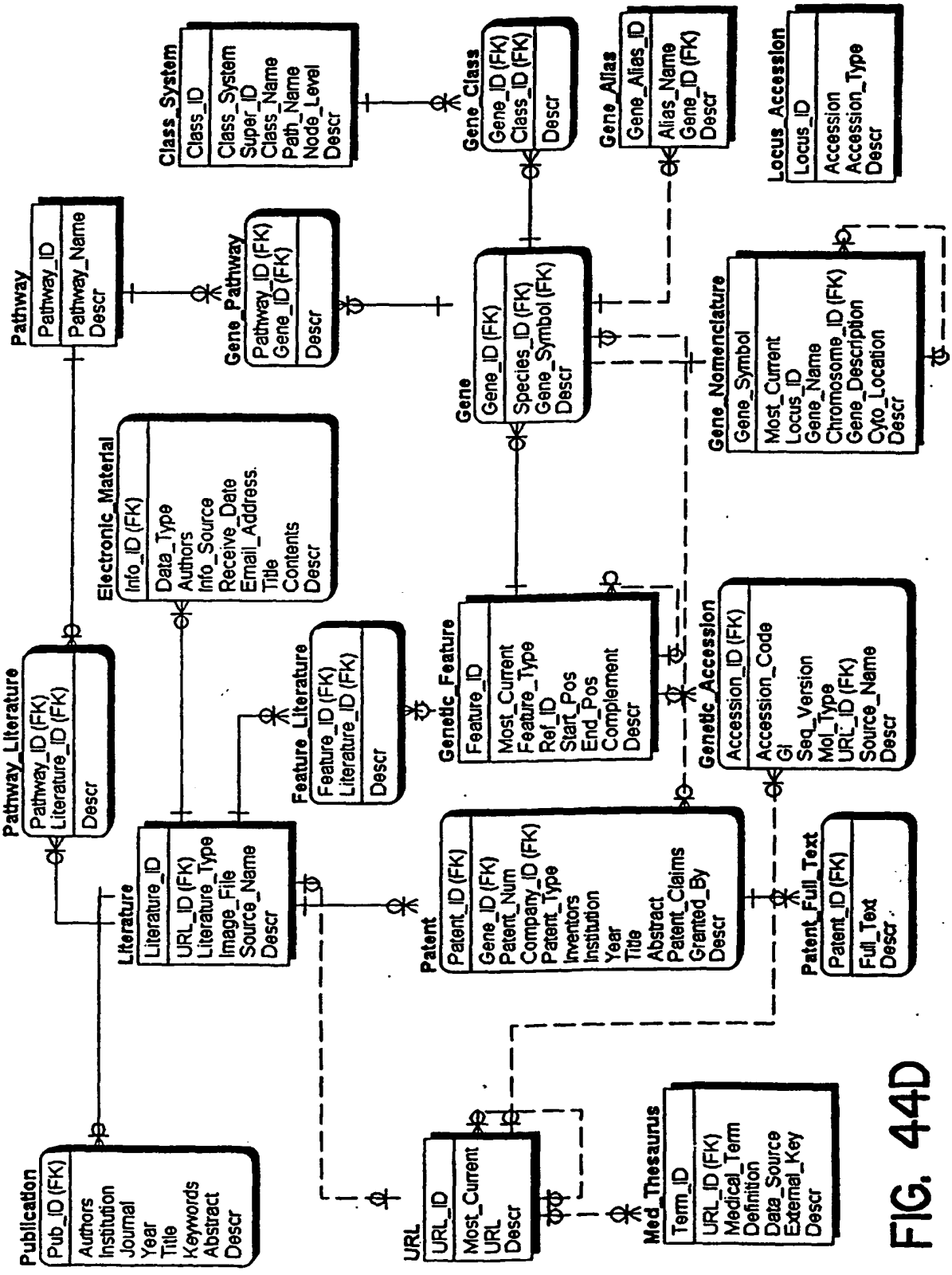

Class_System
Class_ID
Class_System
Super_ID
Class_Name
Path_Name
Node_Level
Descr
Gene_Class
Gene_ID (FK)
Class_ID (FK)
Descr
Gene_Alias
Gene_Alias_ID
Alias_Name
Gene_ID (FK)
Descr
Locus_Accession
Locus_ID
Accession
Accession_Type
Descr
Pathway
Pathway_ID
Pathway_Name
Descr
Gene_Pathway
Pathway_ID (FK)
Gene_ID (FK)
Descr
Gene
Gene_ID (FK)
Species_ID (FK)
Gene_Symbol (FK)
Descr
Gene_Nomenclature
Gene_Symbol
Most_Current
Locus_ID
Gene_Name
Chromosome_ID (FK)
Gene_Description
Cyto_Location
Descr
Electronic_Material
Info_ID (FK)
Data_Type
Authors
Info_Source
Receive_Date
Email_Address.
Title
Contents
Descr
Genetic_Feature
Feature_ID
Most_Current
Feature_Type
Ref_ID
Start_Pos
End_Pos
Complement
Descr
Genetic_Accession
Accession_ID (FK)
Accession_Code
GI
Seq_Version
Mol_Type
URL_ID (FK)
Source_Name
Descr
Feature_Literature
Feature_ID (FK)
Literature_ID (FK)
Descr
Pathway_Literature
Pathway_ID (FK)
Literature_ID (FK)
Descr
Literature
Literature_ID
URL_ID (FK)
Literature_Type
Image_File
Source_Name
Descr
Patent
Patent_ID (FK)
Gene_ID (FK)
Patent_Num
Company_ID (FK)
Patent_Type
Inventors
Institution
Year
Title
Abstract
Patent_Claims
Granted_By
Descr
Patent_Full_Text
Patent_ID (FK)
Full_Text
Descr
Publication
Pub_ID (FK)
Authors
Institution
Journal
Year
Title
Keywords
Abstract
Descr
URL
URL_ID
Most_Current
URL
Descr
Med_Thesaurus
Term_ID
URL_ID (FK)
Medical_Term
Definition
Data_Source
External_Key
Descr

FIG. 44D

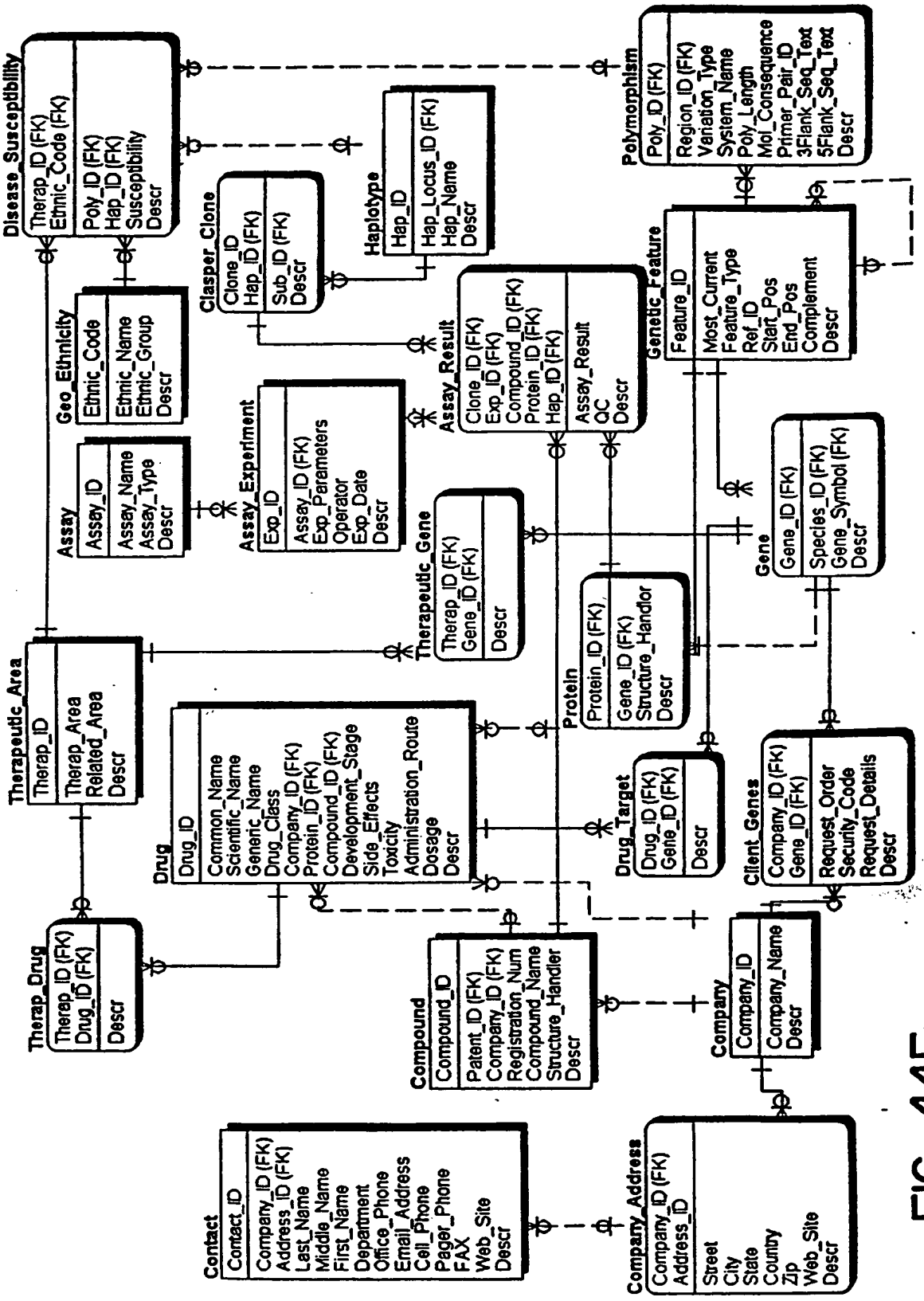
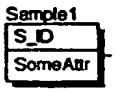

Disease_Susceptibility
Therap_ID (FK)
Ethnic_Code (FK)
Poly_ID (FK)
Hap_ID (FK)
Susceptibility
Descr
Polymorphism
Poly_ID (FK)
Region_ID (FK)
Variation_Type
System_Name
Poly_Length
Mol_Consequence
Primer_Pair_ID
3Flank_Seq_Text
5Flank_Seq_Text
Descr
Haplotype
Hap_ID
Hap_Locus_ID (FK)
Hap_Name
Descr
Clasper_Clone
Clone_ID
Hap_ID (FK)
Sub_ID (FK)
Descr
Geo_Ethnicity
Ethnic_Code
Ethnic_Name
Ethnic_Group
Descr
Assay_Result
Clone_ID (FK)
Exp_ID (FK)
Compound_ID (FK)
Protein_ID (FK)
Hap_ID (FK)
Assay_Result
QC
Descr
Genetic_Feature
Feature_ID
Most_Current
Feature_Type
Ref_ID
Start_Pos
End_Pos
Complement
Descr
Assay
Assay_ID
Assay_Name
Assay_Type
Descr
Assay_Experiment
Exp_ID
Assay_ID (FK)
Exp_Parameters
Operator
Exp_Date
Descr
Therapeutic_Gene
Therap_ID (FK)
Gene_ID (FK)
Descr
Gene
Gene_ID (FK)
Species_ID (FK)
Gene_Symbol (FK)
Descr
Therapeutic_Area
Therap_ID
Therap_Area
Related_Area
Descr
Protein
Protein_ID (FK)
Gene_ID (FK)
Structure_Handler
Descr
Drug
Drug_ID
Common_Name
Scientific_Name
Generic_Name
Drug_Class
Company_ID (FK)
Protein_ID (FK)
Compound_ID (FK)
Development_Stage
Side_Effects
Toxicity
Administration_Route
Dosage
Descr
Drug_Target
Drug_ID (FK)
Gene_ID (FK)
Descr
Client_Genes
Company_ID (FK)
Gene_ID (FK)
Request_Order
Security_Code
Request_Details
Descr
Therap_Drug
Therap_ID (FK)
Drug_ID (FK)
Descr
Compound
Compound_ID
Patent_ID (FK)
Company_ID (FK)
Registration_Num
Compound_Name
Structure_Handler
Descr
Company
Company_ID
Company_Name
Descr
Contact
Contact_ID
Company_ID (FK)
Address_ID (FK)
Last_Name
Middle_Name
First_Name
Department
Office_Phone
Email_Address
Cell_Phone
Pager_Phone
FAX
Web_Site
Descr
Company_Address
Company_ID (FK)
Address_ID
Street
City
State
Country
Zip
Web_Site
Descr

FIG. 44E

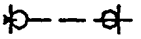
Legend of Figures:

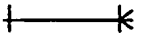


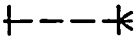
Rectangle Boxes: Tables in the database.

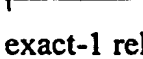
Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

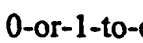
2: Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.

4:  Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.

6:  Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.

8:  Non-identifying parent / child relationship. It represents the not nullable 1-to-1-or-many relationship.

10:  Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.

12:  Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-exact-1 relationship.

14: Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.

FIG. 44F

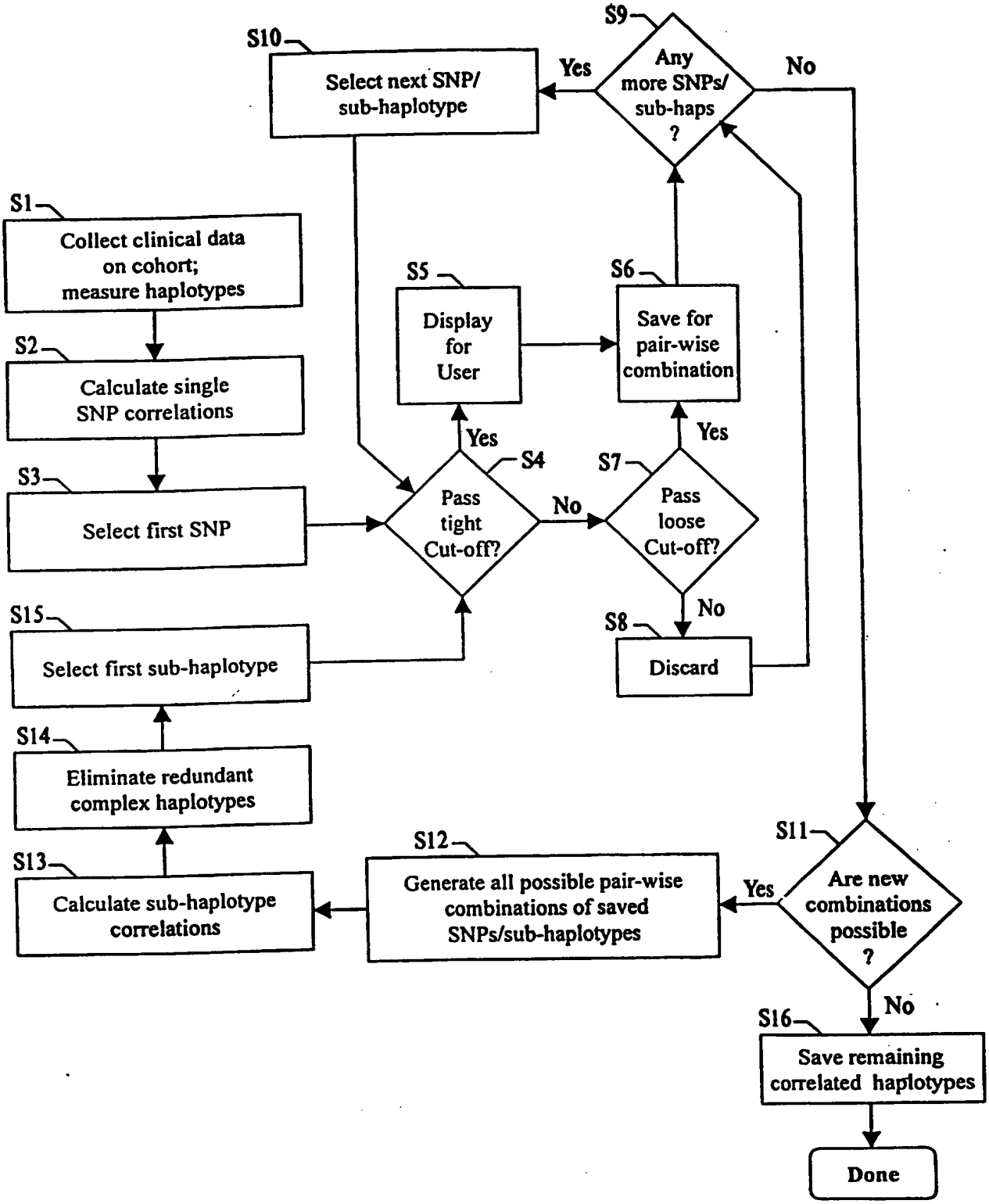

S1
Collect clinical data on cohort; measure haplotypes
S2
Calculate single SNP correlations
S3
Select first SNP
S4
Pass tight Cut-off?
Yes
No
S5
Display for User
S6
Save for pair-wise combination
S7
Pass loose Cut-off?
Yes
No
S8
Discard
S9
Any more SNPs/ sub-haps ?
Yes
No
S10
Select next SNP/ sub-haplotype
S11
Are new combinations possible ?
Yes
No
S12
Generate all possible pair-wise combinations of saved SNPs/sub-haplotypes
S13
Calculate sub-haplotype correlations
S14
Eliminate redundant complex haplotypes
S15
Select first sub-haplotype
S16
Save remaining correlated haplotypes
Done

FIG. 45

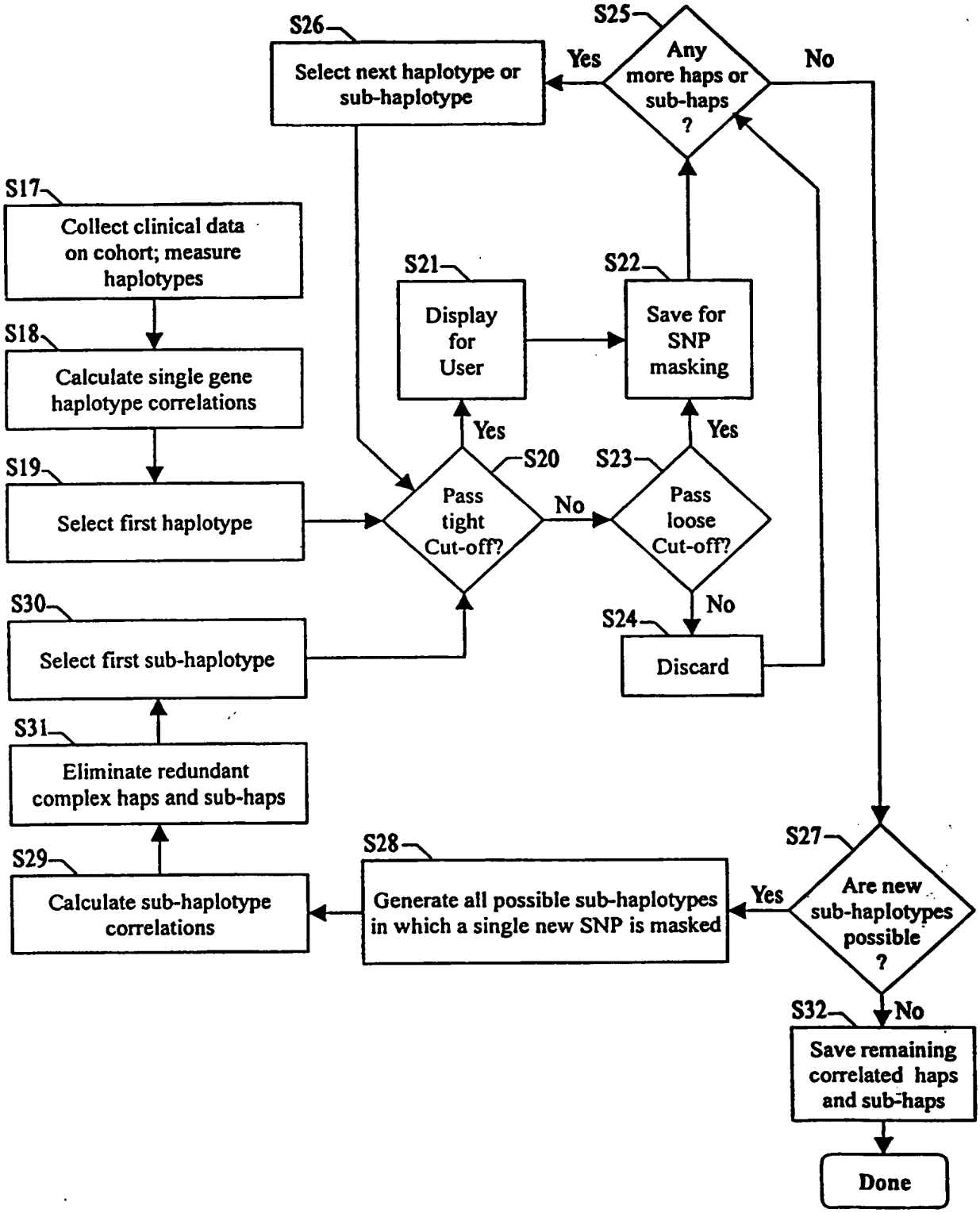

S17
Collect clinical data on cohort; measure haplotypes
S18
Calculate single gene haplotype correlations
S19
Select first haplotype
S30
Select first sub-haplotype
S31
Eliminate redundant complex haps and sub-haps
S29
Calculate sub-haplotype correlations
S28
Generate all possible sub-haplotypes in which a single new SNP is masked
S27
Are new sub-haplotypes possible ?
Yes
No
S32
Save remaining correlated haps and sub-haps
Done
S20
Pass tight Cut-off?
Yes
No
S21
Display for User
S23
Pass loose Cut-off?
Yes
No
S22
Save for SNP masking
S24
Discard
S25
Any more haps or sub-haps ?
Yes
No
S26
Select next haplotype or sub-haplotype

FIG. 46

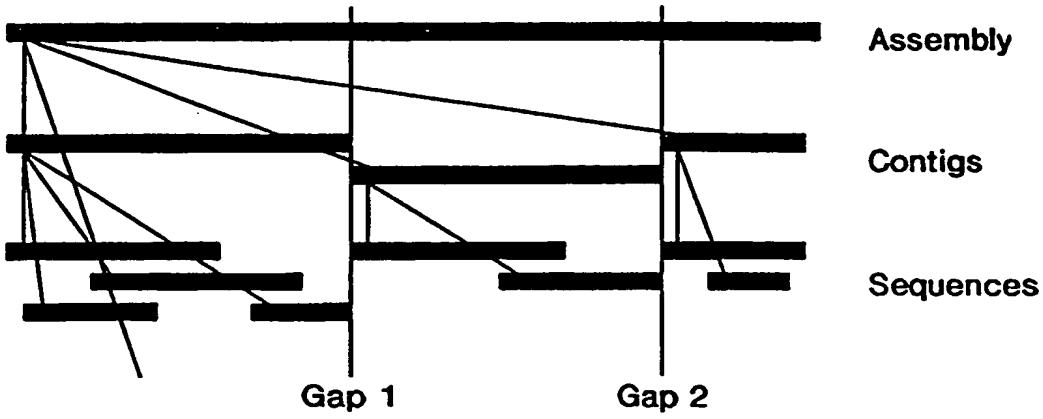

Assembly
Contigs
Sequences
Gap 1
Gap 2

FIG. 47

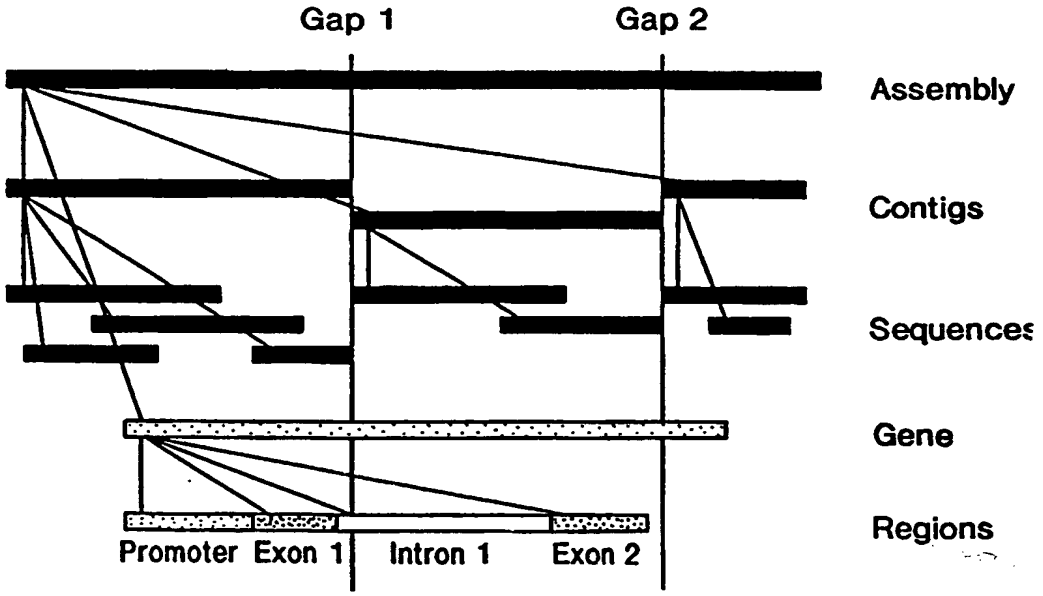

Gap 1
Gap 2
Assembly
Contigs
Sequences
Gene
Regions
Promoter
Exon 1
Intron 1
Exon 2

FIG. 48

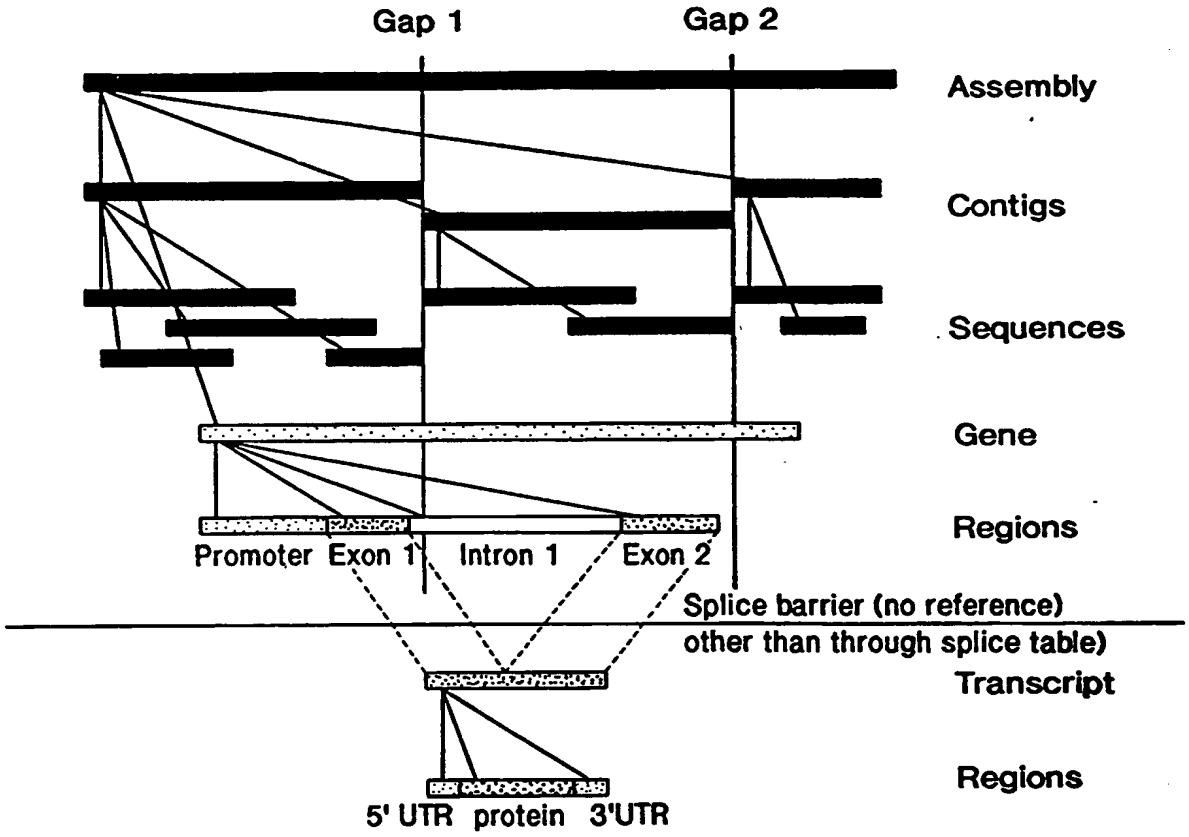

Gap 1
Gap 2
Assembly
Contigs
Sequences
Gene
Regions
Promoter
Exon 1
Intron 1
Exon 2
Splice barrier (no reference)
other than through splice table)
Transcript
Regions
5' UTR
protein
3'UTR

FIG. 49